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**SPECIFICATION**

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TO ALL WHOM IT MAY CONCERN:

15        BE IT KNOWN THAT WE, Stephen W. Michnick, a resident of Montreal, Canada, and  
a citizen of Canada, Marnie L. MacDonald, a resident of Pleasanton, California and citizen of  
USA and Jane Lamerdin, a resident of Livermore, California and citizen of USA; have invented  
certain new and useful improvements in

20        **FRAGMENTS OF FLUORESCENT PROTEINS FOR PROTEIN  
FRAGMENT COMPLEMENTATION ASSAYS**

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## FRAGMENTS OF FLUORESCENT PROTEINS FOR PROTEIN FRAGMENT COMPLEMENTATION ASSAYS

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This application claims the priority benefit under 35 U.S.C. section 119 of U.S. Provisional Patent Application No. 60/461,133 entitled "Fragments of Fluorescent Proteins for Protein Fragment Complementation Assays", filed April 9, 2003, which is in its entirety herein incorporated by reference. This Application is also a continuation-in-part of pending U.S. Application Serial No. 10/353,090 filed January 29, 2003; which application is a continuation of  
10 pending U.S. application No. 10/154,758 filed May 24, 2002; which is a continuation of U.S. Serial No. 09/499,464 filed February 7, 2000; and now U.S. Patent No. 6,428,951; which is a continuation of U.S. Serial No. 09/017,412 filed February 2, 1998; and now U.S. Patent No. 6,270,964.

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### **BACKGROUND OF THE INVENTION**

This invention relates generally to the fields of biology, molecular biology, chemistry and biochemistry. Specifically, the invention is directed to protein-fragment complementation assays (PCAs) based on fluorescent proteins. This invention is directed to methods for the design and  
20 creation of suitable fragment pairs, to the compositions of the fragments, and to combinations suitable for PCA. Preferred embodiments include fragments of mutant fluorescent proteins having properties suitable for biotechnology applications.

The growing list of naturally fluorescent, bioluminescent or phosphorescent proteins includes GFP derived from *Aequorea Victoria*, and a growing number of sequence variants of  
25 GFP with useful properties. The list also includes the red fluorescent protein (RFP) derived from



Discosoma; and the kindling fluorescent protein (KFP1) derived from Anemonia. These proteins are autocatalytic enzymes that are all capable of generating highly visible, efficiently emitting internal fluorophores as a result of endo-cyclization of core amino acid residues. Another common feature of the fluorescent proteins is that the signal is stable, species independent, and does not require any substrates or cofactors for the generation of a signal. These fluorescent proteins are remarkably similar structurally allowing similar principles of protein engineering to be applied across species.

The full-length DNA, and corresponding amino acid sequence of one isotype of GFP ("wild-type GFP") is shown in TABLE 1 and has been fully described and characterized (see e.g. Tsien et al., 1998, Ann. Rev. Biochem. 67: 509-44). The intact protein (Figs. 1 and 2B) generates a strong visible absorbance and fluorescence from a p-hydroxybenzylideneimidazolone chromophore, which is generated by cyclization and oxidation of the protein's own Ser-Tyr-Gly sequence at positions 65 to 67. Newly synthesized fluorescent protein polypeptides need to mature properly before emitting fluorescence. The maturation process involves two steps: folding and chromophore formation. First, the protein folds into a native conformation, and then the internal tripeptide cyclizes and is oxidized. In this regard the fluorescent protein is an enzyme which autocatalyzes the cyclization reaction, requiring only molecular oxygen for completion of the reaction.

A variety of useful mutant versions of the full-length, wild-type GFP have been generated and have been termed 'Aequorea fluorescent protein (AFP) variants' or AFPs. These "mutant fluorescent proteins" have proven to have wide applicability for biology and biotechnology applications as a result of their improved spectral properties. Some of the reported GFP variants are shown in Table 2. By conventional usage, the positions of the mutations (as in Table 2 and

throughout this invention) are denoted relative to the sequence of wild-type GFP (Table 1). Many of these AFPs exhibit vastly improved properties over the original wild-type GFP in terms of signal intensity, generating a fluorescence signal 5 to 30 times that of the wild-type protein. The enhanced GFP (EGFP), which is the basis for nearly all biology applications and for mutant  
5 fluorescent proteins, has improved codon usage for mammalian cells.

Starting with GFP, mutations at the site of the chromophore have been created which result in different color variants. Mutations of the side chains in contact with the chromophore have been shown to further enhance protein folding and brightness. Combinations of mutations have been created that have spectral shifts and that fold more rapidly at 37°C, producing brighter  
10 signals for cell biology applications. The most common spectral variants include the widely-used yellow (YFP/EYFP), cyan (CFP/ECFP) and BFP variants (R.Y. Tsien, 1998, "The Green Fluorescent Protein", in: Annual Reviews of Biochemistry 67: 509-544).

Additional mutants of GFP have been created with unique properties. These include a 'CGFP' variant with an excitation and emission wavelength intermediate between CFP and EGFP  
15 (J. Zhang et al., 2000, "Creating new fluorescent probes for cell biology", Nature Reviews 3: 906-918). The 'citrine' variant of YFP (YFP-Q69M) confers a lower pKa than for previous YFPs, indifference to chloride anion, twice the photostability of previous YFPs, and much better expression at 37°C and in organelles (O. Griesbeck et al., 2001, "Reducing the Environmental Sensitivity of Yellow Fluorescent Protein", J. Biol. Chem 276: 29188-29194).

Several versions of YFP have been created using random mutagenesis. These mutant  
20 proteins have fluorescence intensities 3-30 times brighter than EYFP. They include the so-called super-EYFP (SEYFP) (EYFP-F64L/M153T/V163A/S175G) and 'Venus' (SEYFP-F46L) (T. Nagai et al., 2002, "A variant of yellow fluorescent protein with fast and efficient maturation for

cell-biological applications", *Nature Biotech.* 20: 87-90). Venus contains the novel mutation, F46L, which at 37°C greatly accelerates oxidation of the chromophore, the rate-limiting step of mutation. As a result of the additional SEYFP mutations, Venus SEYFP-F46L also folds well and is relatively tolerant of exposure to acidic or high chloride anion concentrations.

- 5           A photoactivatable form of GFP named PA-GFP (GFP-V163A/T203H) has been reported that, after intense irradiation with 413-nm light, increases fluorescence 100 times when excited by 488-nm light and remains stable for days under aerobic conditions (G.H. Patterson & J. L. Schwartz, "A photoactivatable GFP for selective photolabeling of proteins and cells", *Science* 297: 1873-1877, 2002).

TABLE 1. Full-length Aequorea GFP nucleic acid sequence (716 bp) (SEQ ID No:1) and corresponding amino acid sequence (238 aa) (SEQ ID No:2). Amino acids are numbered at every 5th position. This sequence is for the wild-type protein. In "enhanced" versions of GFP (EGFP, EYFP, ECFP) a valine residue is inserted after the initiating methionine. The valine becomes amino acid # 2 and the remaining amino acids are shifted accordingly. Descriptions of GFP mutants (as in Table 2 and throughout the specifications) refer to the numbering shown below. Alternative fragmentation sites that are the subject of the present invention are shown at the following regions (underlined): amino acid residues 38-40 (region 1); residues 101-103 (region 2); residues 114-118 (region 3); residues 154-160 (region 4); residues 171-175 (region 5); and residues 188-190 (region 6). The positions of specific amino acid residues are shown for Tyrosine 39 (Y39), Aspartate 102 (D102), Glutamine 157 (Q157), Lysine 158 (K158), Aspartate 173 (D173) and Aspartate 190 (D190).

15	atg Met 1	agt Ser	aaa Lys	gga Gly	gaa Glu 5	gaa Glu	ctt Leu	ttc Phe	act Thr	gga Gly 10	gtt Val	gtc Val	cca Pro	att Ile	ctt Leu 15	gtt Val
20	gaa Glu	tta Leu	gat Asp	ggt Gly 20	gat Asp	gtt Val	aat Asn	ggg Gly	cac His 25	aaa Lys	ttt Phe	tct Ser	gtc Val	agt Ser 30	gga Gly	gag Glu
25	ggt Gly	gaa Glu	ggt Gly 35	gat Asp	gca Ala	<u>aca Tyr</u>	<u>tac Tyr</u>	<u>gga Gly</u>	aaa Lys	ctt Leu	acc Thr	ctt Leu	aaa Lys 45	ttt Phe	att Ile	tgc Cys
30	act Thr	act Thr 50	gga Gly	aaa Lys	cta Leu	cct Pro	gtt Val 55	cca Pro	tgg Trp	cca Pro	aca Thr	ctt Leu 60	gtc Val	act Thr	act Thr	ttc Phe
35	tct Ser 65	tat Tyr	ggt Gly	gtt Val	caa Gln	tgc Cys 70	ttt Phe	tca Ser	aga Arg	tac Tyr	cca Pro 75	gat Asp	cat His	atg Met	aaa Lys	cgg Arg 80
40	cat His	gac Asp	ttt Phe	ttc Phe	aag Lys 85	agt Ser	gcc Ala	atg Met	ccc Pro	gaa Glu 90	ggt Gly	tat Tyr	gta Val	cag Gln	gaa Glu 95	aga Arg
45	act Thr	ata Ile	ttt Phe	ttc Phe 100	<u>aaa Lys</u>	<u>gat Asp</u>	<u>gac Asp</u>	ggg Gly	aac Asn 105	tac Tyr	aag Lys	aca Thr	cgt Arg	gct Ala 110	gaa Glu	gtc Val
50	aag Lys	<u>ttt Phe</u>	<u>gaa Glu</u>	<u>ggt Gly</u>	<u>gat Asp</u>	<u>acc Thr</u>	ctt Leu	gtt Val 120	aat Asn	aga Arg	atc Ile	gag Glu	tta Leu 125	aaa Lys	ggt Gly	att Ile
55	gat Asp	ttt Phe 130	aaa Lys	gaa Glu	gat Asp	gga Gly	aac Asn 135	att Ile	ctt Leu	gga Gly	cac His	aaa Lys 140	ttg Leu	gaa Glu	tac Tyr	aac Asn
60	tat Tyr 145	aac Asn	tca Ser	cac His	aat Asn	gta Val 150	tac Tyr	atc Ile	atg Met	<u>gca Ala</u>	<u>gac Asp</u>	<u>aaa Lys</u>	<u>caa Gln</u>	<u>aag Lys</u>	<u>aat Asn</u>	<u>gga Gly</u>
65	atc Ile	aaa Lys	gtt Val	aac Asn	ttc Phe 165	aaa Lys	att Ile	aga Arg	cac His	aac Asn 170	att Ile	gaa Glu	gat Asp	gga Gly	agg Ser	gtt Val
70	caa Gln	cta Leu	gca Ala	gac Asp 180	cat His	tat Tyr	caa Gln	caa Gln	aat Asn 185	act Thr	cca Pro	<u>att Ile</u>	<u>ggc Gly</u>	<u>gat Asp</u>	<u>ggc Gly</u>	cct Pro
75	gtc Val	ctt Leu	tta Leu 195	cca Pro	gac Asp	aac Asn	cat His	tac Tyr 200	ctg Leu	tcc Ser	aca Thr	caa Gln	tct Ser 205	gcc Ala	ctt Leu	tcg Ser
80	aaa Lys	gat Asp 210	ccc Pro	aac Asn	gaa Glu	aag Lys	aga Arg 215	gac Asp	cac His	atg Met	gtc Val	ctt Leu 220	ctt Leu	gag Glu	ttt Phe	gta Val
85	aca Thr 225	gct Ala	gct Ala	ggg Gly	att Ile	aca Thr 230	cat His	ggc Gly	atg Met	gat Asp	gaa Glu 235	cta Leu	tac Tyr	aaa Lys		

**Table 2. Spectral characteristics of the major classes of Aequorea fluorescent proteins (AFPs)**

Mutation	Common name	$\square_{exc}(\epsilon)$	$\square_{cm}(QY)$	Rel. fl. @ 37°C
Class 1, wild-type None or Q80R	Wild type	395-397 (25-30) 470-475 (9.5-14)	504 (0.79)	6
F99S, M153T, V163A	Cycle 3	397 (30) 475 (6.5-8.5)	506 (0.79)	100
Class 2, phenolate anion S65T F64L, S65T F64L, S65T, V163A S65T, S72A, N149K, M153T, I167T	EGFP  Emerald	489 (52-58) 488 (55-57) 488 (42) 487 (57.5)	509-511 (0.64) 507-509 (0.60) 511 (0.58) 509 (0.68)	12 20 54 100
Class 3, neutral phenol S202F, T203I T203I, S72A, Y145F	H9 H9-40	399 (20) 399 (29)	511 (0.60) 511 (0.64)	13 100
Class 4, phenolate anion with stacked $\pi$ -electron system (yellow fluorescent proteins) (YFPs)				
S65G, S72A, T203F S65G, S72A, T203Y S65G, V68L, Q69K S72A, T203Y S65G, V58L, S72A, T203Y S65G, S72A, K79R, T203Y F46L F64L, M153T, V163A, S175G  F46L, F64L, M153T, V163A, S175G  V68L, Q69M  V163A, T203H	EYFP 10C Q69K  10C Topaz  EYFP-F46L SEYFP  SEYFP-F46L (‘Venus’)  ‘Citrine’  PA-GFP	512 (65.5) 508 (48.5) 516 (62)  514 (83.4) 514 (94.5)  515 (78.7) 515 (101)  see: Nagai et al., Nature Biotech. 20: 87-90, 2002  see: Griesbeck et al., J. Biol. Chem 276: 29188-29194 (2001)  see: Patterson et al., Science 297: 1873-1877, 2002	522 (0.70) 518 (0.78) 529 (0.71)  527 (0.61) 527 (0.60)  528 (0.61) 528 (0.56)	6 12 50  58 100  ND ND
Class 5, indole in chromophore (cyan fluorescent proteins) (CFPs)				
Y66W Y66W, N146I, M153T, V163A F64L, S65T, Y66W, N146I, M153T, V163A S65A, Y66W, S72A, N146I, M153T, V163A T203Y	W7  W1B or ECFP W1C  CGFP	436 434 (23.9) 452 434 (32.5) 452 435 (21.2)  see: Sawano & Miyawaki, Nucleic Acid Res. 28: E78 (2000)	485 476 (0.42) 505 476 (0.4) 505 495 (0.39)	— 61  80  100
Class 6, imidazole in chromophore (blue fluorescent proteins) (BFPs)				
Y66H Y66H, Y145F F64L, Y66H, Y145F	BFP P4-3 EBFP	384 (21) 382 (22.3) 380-383 (26.3-31)	448 (0.24) 446 (0.3) 440-447 (0.17-0.26)	18 52 100
Class 7, phenyl in chromophore				
Y66F		360	442	—

**Table 3. Alignment of wild type *Aequorea victoria* GFP and *Aequorea*-derived fluorescent proteins (Zhang et al. 2002). New variants of green fluorescent protein (GFP) (SEQ ID No:2) that encode proteins with altered excitation and emission wavelength properties relative to wild type GFP are aligned. These include the mammalian codon-usage optimized ECFP (cyan) (SEQ ID No:8), EGFP (green) (SEQ ID No:3), (cyan), EGFP (green), and EYFP (yellow) (SEQ ID No:4) variants. Three more recent variants of EYFP include EYFP-Q69M (Citrine) (SEQ ID No:5), super-EYFP (SEYFP) (SEQ ID No:6), and SEYFP-F46L ('Venus') (SEQ ID No:7).**

	GFP	1	-MSKGEELFTGVVPILVELDGDVNGHKFSVSGEGEGDATYGKLTCLKFICTTGKLPVPWPT
	EGFP	1	MV.....
	EYFP	1	MV.....
15	EYFP-Q69M	1	MV.....
	SEYFP	1	MV.....
	SEYFP-F46L	1	MV.....L.....
	ECFP	1	MV.....
20	GFP	60	LVTTFSYGVQCFSRYPDHMKQHDFFKSAMPEGYVQERTIFFKDDGNYKTRAEVKFEQDTL
	EGFP	61	....LT.....
	EYFP	61	....G..L..A.....
	EYFP-Q69M	61	....G..LM..A.....
	SEYFP	61	....LG..L..A.....
25	SEYFP-F46L	61	....LG..L..A.....
	ECFP	61	....LTW.....
30	GFP	120	VNRIELKGIDFKEDGNILGHKLEYNNSHNVYIMADKQKNGIKVNFKIRHNIEDGSVQLA
	EGFP	121	.....
	EYFP	121	.....
	EYFP-Q69M	121	.....
	SEYFP	121	.....T.....A.....G.....
	SEYFP-F46L	121	.....T.....A.....G.....
35	ECFP	121	.....I.....T.....A.....
40	GFP	180	DHYQQNTPIGDGPVLLPDNHYLSTQSALSKDPNEKRDHMLLEFVTAAGITHGMDELYK
	EGFP	181	.....L.....
	EYFP	181	.....Y.....L.....
	EYFP-Q69M	181	.....Y.....L.....
	SEYFP	181	.....Y.....L.....
	SEYFP-F46L	181	.....Y.....L.....
	ECFP	181	.....L.....

Fluorescent proteins from species other than *Aequorea victoria* have also been isolated and characterized. The growing list includes a green fluorescent protein from *Renilla reniformis*, and a number of fluorescent proteins from the coral Anthozoa. These include the red fluorescent protein from *Discosoma* (DsRed) (M.V. Matz et al., 1999, Nature Biotech. 17:969-973) which has been crystallized (Yarbrough et al., 2001, Proc. Natl. Acad. Sci. 98: 462-467) and has found wide applicability as a biology tool. Although the coral fluorescent proteins have only 26-30% sequence identity with *Aequorea* GFP, they are remarkably similar structurally. In particular, the coral fluorescent proteins share the same  $\beta$ -can fold first observed in GFP. All the key secondary

structure elements observed in GFP could be easily detected in the coral proteins in the same arrangements, and remarkable similarity was observed in the stretches forming the "caps" of the can. Key residues thought to be involved in chromophore formation in GFP are also conserved in the coral proteins, including an Arginine at residue 96, the Tyrosine at residue 66 and Glycine at residue 67.

The structural homology of fluorescent proteins among various species means that many of the principles of genetic engineering and protein engineering previously applied to GFP can also be applied to these fluorescent proteins to create variants with desirable properties for biological applications and biotechnology.

The availability of a bright orange-red fluorescent protein with a high quantum yield would be particularly useful for biological studies as it is spectrally distinct from the previously described green, yellow and cyan variants of GFP. DrFP583, commonly known as DsRed, is a 28-kDa polypeptide that has essentially the same chromophore as GFP, which is autocatalytically formed from an internal Gln-Tyr-Gly (residues 66-68) tripeptide. DsRed is remarkably similar structurally to *A. victoria* GFP. In fact, the overall fold of DsRed is virtually identical to GFP, consisting of a slightly irregular 11-stranded beta-barrel (described as a beta can) with a coaxial central helix and alpha-helical caps on the barrel ends. The sequence alignment of the coral fluorescent proteins with *Aequorea* GFP is shown in Table 4.

A number of mutant versions of DsRed have now been described with faster rates of chromophore maturation than the wild-type protein (B.J. Bevis and B.S. Glick, *Nature Biotech.* 20: 83-86, 2002). Importantly, DsRed has recently been engineered into a monomeric form (mRFP) (R.E. Campbell et al., June 11, 2002, "A monomeric red fluorescent protein", *Proc. Natl. Acad. Sci.* 99(12): 7877-7882) which is more useful than the multimeric protein as a reporter.

mRFP1 is a monomer, the signal matures >10-fold faster than for DsRed, and the monomeric protein has minimal emission at wavelengths suitable for excitation of GFP.

A unique GFP-like chromoprotein asCP from the sea anemone *Anemonia sulcata* was recently discovered (Chudakov, D.M., et al. 2003, "Kindling fluorescent proteins for precise in vivo photolabeling". *Nat. Biotechnol.* 21, 191-194). asCP is initially nonfluorescent, but in response to intense green light irradiation it becomes brightly fluorescent (kindles) with emission at 595 nm. Kindled asCP relaxes back to the initial nonfluorescent state with a half-life of <10 seconds. Alternatively, fluorescence can be "quenched" instantly and completely by a brief irradiation with blue light. A mutant (asCP A148G, or KFP1) has been generated which is capable of unique irreversible photoconversion from the nonfluorescent to a stable bright-red fluorescent form that has 30 times greater fluorescent intensity than the unkindled protein. This "kindling fluorescent protein" can be used for precise in vivo photolabeling to track the movement of cells, organelles and proteins.

Fluorescent proteins have proven to be useful reporters for monitoring gene expression and protein localization in vivo and in real time (J.M. Tavaré et al., 2001, *J. Endocrinol.* 170: 297-306; Thastrup et al., US 6,518,021). Such assays measure cellular events linked to individual proteins, as compared with binary or higher-order events. A number of other useful applications of fluorescent proteins have been described, including the construction of biochemical sensors and the creation of innovative fusion constructs to analyze protein dynamics in living cells. For the measurement of bimolecular events, FRET (fluorescence resonance energy transfer) or BRET (bioluminescence resonance energy transfer) assays have been well described (A. Miyawaki & R. Tsien, 2000, *Methods in Enzymology* 327: 472-500; G.W. Gordon et al., 1998, *Biophys. J.* 74: 2702-2713). GFP, BFP, CFP and RFP have been used in FRET or



BRET assays to detect protein-protein interactions, monitor protease activity, and create calcium indicators, among other uses.

It is important to note that all the above-mentioned applications rely upon tagging of proteins of interest with a functional, full-length (or substantially full-length) fluorescent protein (lumiphore). None of the references cited above describe compositions or uses of fragments of fluorescent proteins.

Protein-fragment complementation assays (PCA) represent a general method for the construction of assays for the detection and quantitation of biomolecular and drug interactions (J.N. Pelletier, J.N., Remy, I. and Michnick, S.W. 1998, Protein-Fragment complementation Assays: a general strategy for the *in vivo* detection of Protein-Protein Interactions, J. Biomolecular Techniques 10:32-19; Remy, I., Pelletier, J.N., Galarneau, A. & Michnick, S.W. 2002, Protein Interactions and Library Screening with Protein Fragment Complementation Strategies, in: Protein-protein Interactions: A Molecular Cloning Manual, Cold Spring Harbor Laboratory Press Chapter 25, 449-475; Michnick, S.W., Remy, I., C.-Valois, F.X., Vallee-Belisle, A., Galarneau, A. & Pelletier, J.N., 2000, Detection of Protein-Protein Interactions by Protein Fragment Complementation Strategies, Parts A and B, in: Methods in Enzymology 328:208-230.; J. N. Pelletier & S. W. Michnick. ,1997, A Strategy for Detecting Protein-Protein Interactions *in vivo* Based on Protein Fragment Complementation. *Protein Engineering*, 10(Suppl.): 89.).

PCA involve the oligomerization-assisted complementation of fragments of a reporter protein such as a monomeric enzyme, a fluorescent protein, luminescent protein or phosphorescent protein. Dimeric and multimeric enzymes can also be used in PCA, however, monomeric proteins are preferred. As described by Michnick et al. (US 6,270,964) the ideal

properties of a protein suitable for PCA are: 1) a protein or enzyme that is relatively small and monomeric; 2) for which there is a large literature of structural and functional information; 3) for which simple assays exist for the reconstitution of the protein or activity of the enzyme; and 4) for which overexpression in eukaryotic and prokaryotic cells has been demonstrated.

5           Figure 1 of US 6,270,964 shows a general description of a PCA. The gene for a protein or enzyme is rationally dissected into two or more fragments. Using molecular biology techniques, the chosen fragments are subcloned, and to the 5' ends of each, proteins that either are known or thought to interact are fused. Co-transfection or transformation of these DNA constructs into cells is then carried out. Reassembly of the probe protein or enzyme from its  
10 fragments is catalyzed by the binding of the test proteins to each other, and reconstitution is observed with some assay. It is crucial to understand that these assays will only work if the fused, interacting proteins catalyze the reassembly of the protein or enzyme. That is, observation of reconstituted protein or enzyme activity must be a measure of the interaction of the fused proteins.

15           US 6,270,964 taught the principles, methods and applications of PCAs for a large number of useful reporters that can generate a fluorescent signal (see Table 1). Example 3 of that patent describes various embodiments of PCAs including a number of specific reporters suitable for PCA. Details were described for glutathione-S-transferase, firefly luciferase, xanthine-guanine phosphoribosyl transferase (XPRT), diaphorase, adenosine deaminase, bleomycin binding  
20 protein, hygromycin-B-phosphotransferase, histidinol NAD<sup>+</sup>-oxidoreductase and Aequorea green fluorescent protein (GFP). Table 1 of US 6,270,964 described an even larger list of other reporters meeting the criteria for PCA.

In Example 3 of US 6,270,964 a PCA based on GFP was described including its properties and advantages: "GFP from *Aequorea victoria* is becoming one of the most popular protein markers for gene expression. This is because the small, monomeric 238 amino acids protein is intrinsically fluorescent due to the presence of an internal chromophore that results from the autocatalytic cyclization of the polypeptide backbone between residues Ser65 and Gly67 and oxidation of the bond of Tyr 66. The GFP chromophore absorbs light optimally at 395 nm and possesses also a second absorption maximum at 470 nm. This bi-specific absorption suggests the existence of two low energy conformers of the chromophore whose relative population depends on the local environment of the chromophore. A mutant Ser65Thr that eliminates isomerization results in a 4 to 6 times more intense fluorescence than the wild type. Recently the structure of GFP has been solved by two groups, making it a candidate for a structure-based PCA design which we have begun to develop. As with the GST assay we are doing all of our initial development in *E. Coli* with GCN4 leucine zipper-forming sequences as oligomerization domains. Direct detection of fluorescence by visual observation under broad spectrum UV light will be used. We will also test this system in COS cells, selecting for co-transfectants using fluorescence activated cell sorting." The issued claims of US 6,270,964, US 6,294,330 and US 6,428,951 include fluorescent proteins in addition to other reporter classes. PCAs have been used to screen diverse peptide libraries (J.N. Pelletier, et al., 2000, *Nature Biotech.* 17: 683-690) and cDNA or antibody libraries (E. Moessner et al., 2001, *J. Mol. Biol.* 308: 115-122; I. Remy et al., submitted for publication); to quantify the association constants of protein domains such as parallel and anti-parallel leucine zipper-forming sequences (K.M. Arndt et al., 2000, *J. Mol. Biol.* 295: 627-639; I. Ghosh et al., 2000, *J. Am. Chem. Soc.* 122:5658-5659); to detect the drug-induced association and dissociation of protein complexes (I. Remy and

S.W. Michnick, 1999, Proc Natl Acad Sci USA 96: 5394-5399); to measure the ligand-induced activation of cellular receptors (I. Remy et al., 1999, Science 283: 990-993); to study transcription factor complexes in live cells (R. Subramaniam et al., 2001, Nature Biotech. 19: 769-772, 2001); to quantitate elements of signal transduction pathways in real time (I. Remy and S.W. Michnick, 2001, Proc Natl Acad Sci USA, 98: 7678-7683, 2001; A. Galarneau et al., 2002, Nature Biotech. 20: 619-622); and to pinpoint the subcellular locations of protein-protein complexes (I. Remy and S.W. Michnick, 2001, Proc Natl Acad Sci USA 98: 7678-7683; R. Subramaniam et al., 2001, Nature Biotech., 19: 769-772; C.-D. Hu et al., Molecular Cell 9: 789-798, 2002; H. Yu et al., submitted for publication).

Subsequent to our inventions describing the use of GFP for PCA, Ghosh et al. (J. Am. Chem. Soc 122:5658-5659, 2000; US 2002/0146701) used a GFP PCA to study GCN4 leucine zipper oligomerization in a manner originally proposed by Michnick et al. They showed antiparallel leucine zipper-directed reassembly of GFP fragments in bacteria. A single GFP variant was chosen for these studies and a single fragmentation site was used. The authors did not disclose additional principles or methods for fragmenting a fluorescent protein based on rational design beyond the principles first described in Michnick et al. (e.g. US 6,270,964). Moreover, other than the fragment pair used in the leucine zipper study, Ghosh and coworkers did not disclose specific assay compositions useful for PCA.

Hu et al. (Molecular Cell 9: 789-798, 2002) described a PCA based on a yellow variant of GFP, where the fragments of YFP were fused either to parallel leucine zippers or to Rel family proteins. However, additional principles and methods of engineering fluorescent proteins, and fragment compositions, were not described by Hu and coworkers. Moreover, the prior art is silent on the topic of whether mutations known to affect the properties of intact fluorescent

proteins would confer similar properties on polypeptide fragments used for PCA.

Since fluorescent protein PCAs do not depend upon external cofactors or substrates for signal generation, they are particularly useful for the construction of cell-based assays. A suite of fluorescent protein PCAs would enable a large number of useful assays with differing spectral properties. For example, fluorescent proteins with high quantum yields could be engineered into PCA fragments to allow detection of rare events within cells, such as complexes between proteins expressed at very low levels, or low-affinity complexes between enzymes and their substrates. In addition, PCAs with red-shifted emissions would provide improved signal to noise relative to cellular autofluorescence which often occurs in the green channel. Importantly, fragments generating different color PCAs could be combined to allow simultaneous monitoring of two, three, or more cellular events (multicolor PCA). Finally, fluorescent protein PCAs could be used to create multicolor arrays for rapid diagnostics. For example, multicolor arrays based on antibodies binding to different antigens would allow the rapid and simultaneous detection of bio-warfare agents.

## **OBJECTS AND ADVANTAGES OF THE INVENTION**

It is an object of the present invention to provide methods for designing and engineering fluorescent protein fragments and mutant fragments for PCA.

It is a further object of the invention to describe a large number of fragment pairs and compositions useful for PCA.

Another object of the invention is to teach that any useful sequence variant of an intact fluorescent protein can be engineered into the PCA fragments, generating assays with a variety of spectral and physical properties.

A further object of the invention is to provide compositions of PCA fragments, incorporating a wide range of mutations that confer useful properties.

A still further object of the invention is to provide multicolor PCAs'.

The advantage of the invention is the ability to create 'designer' PCAs with a range of  
5 useful properties for a variety of applications.

### SUMMARY OF THE INVENTION

The present invention relates to a composition comprising complementary fragments of a protein, said fragments generating an optically detectable signal when associated.

10 The invention also relates to fragments derived from fluorescent proteins and mutant fluorescent proteins.

The instant invention also describes complementary fragments of mutant fluorescent proteins which differ from the corresponding fragments of the wild-type protein by at least one amino acid.

15 The invention further relates to complementary fragments selected from the group consisting of: Seq. ID NO: 20 to Seq. ID NO: 1067.

The invention also describes a composition selected from Seq. ID NO: 20 to Seq. ID NO: 1067 which are further fused to a separate molecule.

20 The invention also provides a composition comprising complementary fragments of a mutant protein, said fragments generating an optically detectable signal when associated, wherein each fragment is fused to a separate molecule.

The invention is further directed to protein fragment complementation assays for the detection of molecular interactions comprising a reassembly of separate fragments from an

optically detectable protein wherein reassembly of the fragments is operated by the interaction of molecular domains fused to each fragment, wherein reassembly of the fragments is independent of other molecular processes and wherein said reassembly is detected by means of reconstitution of activity of said optically detectable protein.

5           The invention also provides a method for detecting biomolecular interactions said method comprising: (a) selecting an appropriate optically detectable protein; (b) effecting fragmentation of said optically detectable protein such that said fragmentation results in reversible loss of protein function; (c) fusing or attaching fragments of said optically detectable protein separately to other molecules; (d) reassociating said protein fragments through interactions of the molecules  
10   that are fused or attached to said fragments; and (e) detecting the resulting optical signal.

          The present invention also concerns the design and engineering of protein-fragment complementation assays based on fluorescent proteins. Methods for fragmenting fluorescent proteins and creating mutant fragments with specific properties are described, based on fluorescent proteins derived from Aequorea, Anthozoa and Anemonia species. Finally, a large  
15   number of fragment compositions and fragment pairs are provided that incorporate mutations with useful properties generating green, yellow, cyan, blue or red signals. Detailed examples of fluorescent protein PCAs are shown with numerous mutants of Aequorea fluorescent proteins, demonstrating the engineering principles and showing that mutations conferring useful properties to the full-length protein can also be conferred to the fragments. The invention also provides  
20   methods and compositions for the construction of multi-color PCAs.

#### **BRIEF DESCRIPTION OF THE DRAWINGS**

Figures 1a and 1b show regions in which Aequorea fluorescent proteins can be

fragmented. Figure 1A shows six alternative loops (asterisked) where fragmentation can be effected relative to the linear sequence. Figure 1B shows specific amino acid residues at the sites (see arrows), relative to the three-dimensional structure of the protein; amino acid residues at the fragmentation sites are numbered relative to wild-type GFP.

5        Figure 2 depicts the strategy for design and creation of a fluorescent protein-fragment complementation assay.

Figure 3 shows photomicrographs of PCA results in live cells, depicting the relative fluorescent intensities achieved with PCAs based on two variants of *A. victoria* (GFP PCA and YFP PCA); several different protein-protein complexes were evaluated by fluorescence  
10    microscopy 24 hours after transient transfection.

Figure 4 shows PCAs based on fragment pairs generated from several alternative fragmentation sites as depicted in Fig. 1a and 1b.

Figure 5 shows that specific mutations enhance the fluorescent intensities of reassembled fragments, comparing two sequence variants of a YFP PCA that differ by two  
15    amino acids; the proteins fused to the complementary fragments are the protein kinases MEK and ERK.

Figure 6 shows the bright signal generated by a super-enhanced PCA (panel a) with mutations that enhance the folding of YFP fragments as compared with a non-enhanced PCA (panel b). The sub-cellular location of protein-protein complexes can also be seen by  
20    fluorescence microscopy. Individual YFP fragments are incapable of fluorescing (c and d).

Figures. 7a and 7b shows the effect of engineering additional mutations into fragments in order to enhance the fluorescent intensities of the final PCA, creating an intense fluorescent PCA



(IFP PCA) and allowing for the detection of protein-protein interactions with low (nanogram to sub-nanogram) quantities of DNA.

Figure 8 shows that PCA based on mutant fragments of fluorescent proteins can be used in high-content assays, for example, to detect a change in subcellular localization of protein-protein complexes upon stimulation of living cells by a cytokine as shown here for p65/p50.

Figure 9 demonstrates a spectrally shifted PCA based on mutant fluorescent protein fragments generating a blue signal in the presence of a protein-protein interaction

Figure 10 demonstrates multi-color PCA, wherein a single fusion protein (p65 in this example) tagged with a fragment corresponding to the C-terminus of a fluorescent protein is capable of generating two different fluorescent PCAs in the same cell depending upon the amino acid sequence of the reporter fragment fused to the proteins that interact with the first protein. Multi-color PCAs allow for the detection and quantification of different protein-protein complexes within the same cells.

## DETAILED DESCRIPTION OF THE INVENTION

Fluorescent proteins are particularly attractive for PCAs because they require no external substrates or probes for the generation of the fluorescent signal. However, fluorescent proteins present certain design challenges because of their unique structure and the requirement for internal formation of an active chromophore for generation of the fluorescent signal. The present invention encompasses the design criteria for fragmentation of a fluorescent protein, which are described below.

Figure 2 describes the steps involved in creating a PCA based on a fluorescent protein. The first step is the selection of a fluorescent protein and its corresponding DNA sequence. Any

fluorescent protein can be used for PCA based on the design principles that are the subject of the present invention. The choice of a fluorescent protein depends on the desired wavelength, instrumentation, and sensitivity required for the assay of interest. DNA fragments of the selected reporter are then made, using one of the methods described herein. In the first example, we describe the use of rational design to determine where to fragment a fluorescent protein. Because the fluorescent proteins have similar structures, we first describe the design principles for the example of *A. victoria* GFP.

GFP is an 11-stranded  $\beta$ -barrel with the highly unusual feature of having an  $\alpha$ -helix that is thread through the central axis of the  $\beta$ -barrel (Ormo et al., *Science* 273:1392–95, 1996; F. Yang et al., *Nat. Biotechnol.* 14:1246–5121, 1996; R. Heim et al., *Nature* 373: 663-64, 1995).

Fig. 1A shows a two-dimensional view of the protein; the 11 strands of the barrel are shown in relation to the central alpha-helix, and the amino acid positions at the ends of the barrel are numbered. Fig. 1B shows the 3-dimensional structure of the folded protein; the positions of specific residues at the loops are noted (all numbering is relative to the wild-type GFP). The chromophore is attached to the  $\alpha$ -helix and is buried almost completely in the center of the  $\beta$ -barrel cylinder. Almost all the primary sequence is used to build the  $\beta$ -barrel and axial helix. The chromophore is a *p*-hydroxybenzylidene-imidazolinone formed from residues 65–67, which are Ser(Thr)-Tyr-Gly in the native protein (1,2). The chromophore is a 4-(*p*-hydroxybenzylidene)imidazolidin-5-one attached to the peptide backbone through the 1- and 2-positions of the ring. First, GFP folds into a nearly native conformation, then the imidazolinone is formed by nucleophilic attack of the amide of Gly67 on the carbonyl of residue 65, followed by dehydration. Finally, molecular oxygen dehydrogenates the C $\alpha$ -C $\beta$  bond of residue 66 to put its aromatic group into conjugation with the imidazolinone (3).

There are obvious features of the structure that should not be disrupted and therefore, by default, alternatives to such regions are chosen for fragmentation. The design criteria for fluorescent protein PCAs include the following:

(1) Fragmentation is made in  $\beta$ -turns or loops at the extreme ends of individual strands so as not to disrupt the barrel structure. Preferred regions for fragmentation are shown in Fig. 1A, with specific amino acids corresponding to the regions shown in the 3-dimensional structure in Fig. 1B.

(2) The chromophore is deeply buried in the  $\beta$ -barrel. It is likely that this is required to isolate the chromophore coding sequence, both to assure efficient formation of the chromophore and to maintain both rigid conformation and coordination to the side chains of other amino acids that provide GFP with its unique spectral characteristics. Isolation of the chromophore from solvent is maintained both by being embedded in the  $\beta$ -barrel and also by barrel “capping” structures at either end of the barrel. These caps include: (a) Cap at N-terminus of internal helix: Residues 19-30 strand; Residues 133-143 hairpin; Residues 50-57 (This is the N-terminus of the internal helix); and (b) Cap at C-terminus of internal helix: Residues 1-10, helix; Residues 77-98, helix; Residues 191-197, strand. Neither of these regions should be disrupted.

Based on these criteria the optimal fragmentation regions are shown in Figure 1a relative to the linear model of the GFP structure. Fragmentation can be effected in one of the loops comprising amino acid residues 38-40 (region 1); amino acids 101-103 (region 2); amino acids 114-118 (region 3); amino acids 154-160 (region 4); amino acids 171-175 (region 5); or amino acids 188-190 (region 6). Fragmentation can be effected at one of the amino acids within those regions. It will be obvious to one skilled in the art that the exact residue at which the fragmentation is effected may vary within the designated loops without having a significant

impact on the ability of the fragments to fold and reconstitute an active structure, as long as the design criteria described above and in US 6,270,964 are followed. To prove the design principle, we present examples (Figure 4) of successful PCA construction based on fragmentation of YFP at three different amino acids selected from the regions listed above.

5 While fragmentation of proteins for PCA is generally based on rational dissection of the polypeptide chain as described in the present invention, a number of other engineering approaches can be used that will be well known to one skilled in the art. For example, we have previously proposed an alternative approach based on the use of 5' exonucleases to generate libraries of fragments to search for optimal pairs (Michnick, et al. 6,270,964).

10 In the present invention we generated fragments of the full-length cDNA for GFP using PCR to amplify fragments of interest. Alternatively, oligonucleotides encoding fragments can simply be synthesized using standard oligonucleotide synthesis techniques; this approach was taken to generate a PCA based on a cyan fluorescent protein (Figure 9). In a preferred embodiment, mutant fragments of a fluorescent protein are used, having properties tailored to the  
15 biological application and the instrumentation to be used. To generate mutant fragments, as described below in detail, we utilized site-directed mutagenesis of GFP in order to obtain fragments that when reconstituted would have altered fluorescence properties or superior folding or maturation rates and stabilities. Site-directed mutagenesis is achieved by any of a number of approaches that are well known to one skilled in the art (see MM Ling & BH Robinson, 1997,  
20 Approaches to DNA mutagenesis: an overview. Anal Biochem 254:157-78). Selected examples of such methods are provided here; however, these examples are not intended to be limiting for the practice of this invention. Suitable methods could include combinations of random mutagenesis and directed evolution or DNA shuffling schemes (A.L. Kurtzman et al., 2001,

Advances in directed protein evolution by recursive genetic recombination: applications to therapeutic proteins, *Curr Opin Biotechnol* 2001 Aug;12(4):361-70; SW Santoro et al., 2002, Directed evolution of the site specificity of Cre recombinase. *Proc Natl Acad Sci U S A* 2002 99:4185-90; Z. Shao et al., 1996, Engineering new functions and altering existing functions, *Curr Opin Struct Biol* 6:513-8; S. Harayama, 1998, Artificial evolution by DNA shuffling, *Trends Biotechnol* 1998, 16:76-82); assembly PCR or gene synthesis approaches (WP Stemmer et al., 1995, Single-step assembly of a gene and entire plasmid from large numbers of oligodeoxyribonucleotides, *Gene* 164(1):49-53; RM Horton et al. 1993, Gene splicing by overlap extension. *Methods Enzymol.* 217:270-9), or fragmentation by exo- or endo-nuclease digestion (M. Kitabatake and H. Inokuchi, 1993, A simplified method for generating step-wise deletions using PCR, *Gene* 123:59-61; S. Henikoff, 1990, Ordered deletions for DNA sequencing and in vitro mutagenesis by polymerase extension and exonuclease III gapping of circular templates, *Nucleic Acids Res* 18(10):2961-6). A particularly powerful method is based on 5'-template-assisted long-range plasmid polymerization as exemplified by a number of commercial mutagenesis kits, for example the QuickChange™ system (Stratagene). In addition, various forms of directed evolution based on DNA shuffling could also be used to generate completely novel PCAs.

Once the DNA fragments F1 and F2 of the gene encoding the fluorescent protein are generated, each fragment is individually fused in frame with a gene encoding a protein or polypeptide of interest in a suitable expression vector. A variety of standard or novel expression vectors can be chosen based on the cell type and desired expression level; such vectors and their characteristics will be well known to one skilled in the art. Optimally, a flexible linker, such as that described in Example 1 below, is fused between the fluorescent protein fragment and the

gene of interest to facilitate fragment complementation. Therefore, each expression vector codes for a fusion protein consisting of an operably linked gene of interest, a flexible linker, and either F1 or F2 of the chosen fluorescent protein. As shown in Figure 2, since either F1 or F2 can be fused to the gene of interest and the orientation of the fusion can be either 5' or 3' relative to the gene of interest, four different DNA constructs are possible for any single gene of interest. (It should be noted that if the fluorescent protein fragment is at the 5' end of the construct, it will be preceded by an initiating methionine (atg codon), whereas if the fragment is at the 3' end of the construct, the gene of interest will be preceded by the initiating methionine (atg codon)). Therefore, the invention covers not only F1 fragments that have a naturally occurring initiating methionine, but also the same F1 fragments that have been modified to remove the initiating methionine when the F1 fragment is to be at the 3' end of the construct. Similarly, the invention covers F2 fragments that naturally do not begin with an initiating methionine, but also those same F2 fragments that have been modified include an initiating methionine when the F2 fragment is to be at the 5' end of the construct.

To generate the PCA for a pair of proteins A and B, constructs encoding A and B fused separately to complementary fluorescent protein fragments F1 and F2 are co-transfected into cells. If proteins A and B interact, fragments F1 and F2 are brought into close proximity where they are capable of folding and reconstituting an active chromophore. The fluorescent signal can then be measured by a variety of standard methods, including fluorescence spectroscopy, flow cytometry (FACS), or microscopy. All of these methods can be used in automated, high-throughput formats using instrumentation well known to those skilled in the art. As described below, novel multicolor fluorescent PCAs can also be generated by using more than two construct pairs simultaneously. Finally, although it is expedient to carry out the engineering and

construction of PCAs at the DNA level and then either allow a cell to produce the fusion proteins, it is not essential. For example, fusion proteins can be made in vitro using in vitro expression techniques that are well known to those skilled in the art. In addition, for in vitro PCAs, fusion polypeptides could be produced synthetically by peptide synthesis, or by ligation  
5 of peptide fragments encoding molecules of interest to create peptide fusions with the fluorescent protein fragments.

The structural homology amongst fluorescent proteins from various marine organisms enables the same design criteria described for GFP to be applied to other fluorescent proteins such as those recently described from *Discosoma* and from *Anemonia*. Therefore, in addition to  
10 GFP variants we present additional PCAs based on fragments of the monomerized Red Fluorescent Protein (mRFP1, derived from DsRed); and a fluorescent protein KFP1 that can be transiently activated (kindled) by irradiation of the chromophore at specific wavelengths based on the fluorescent protein 'asCP' from *Anemonia sulcata*. (Chudakov, D. M., Belousov, et al. 2003, Nat Biotechnol 21, 191-194). In both cases the fluorescent proteins are homologues of  
15 GFP at the amino acid level.

The red-shifted fluorescent PCAs that are the subject of this invention will be particularly useful for biological applications in which there is significant auto-fluorescence in the green channel. For example, red-shifted PCAs will be particularly useful for cDNA library screening applications using flow sorting. In this case the positive cell population expressing a protein-  
20 protein complex detected by an RFP PCA will be shifted away from the background population, readily allowing flow sorting of the positive cells.

DsRed from *Discosoma* has been demonstrated to be a structural homologue of GFP. DsRed is a 28-kDa polypeptide that has essentially the same chromophore as GFP, which is

auto-catalytically formed from an internal Gln-Tyr-Gly (residues 66-68) tripeptide. DsRed is remarkably similar structurally to A. victoria GFP. In fact, the overall fold of DsRed is virtually identical to GFP, consisting of a slightly irregular 11-stranded beta-barrel (described as a beta can) with a coaxial central helix and alpha-helical caps on the barrel ends. The novel fragments that are the subject of this invention are based directly on examining of the RFP structure (Wall, M. A., et al., The structural basis for red fluorescence in the tetrameric GFP homolog DsRed, Nat Struct Biol 7, 1133-1138 (2000)) and using the rational design criteria described above for fragmentation of GFP. The amino acid sequence of mRFP1 is shown in Table 5 aligned with the sequence of A. Victoria GFP, showing alignment of the alternative fragmentation sites. The present invention encompasses nucleic acid sequences and polypeptide fragments generated by fragmentation of mRFP1 at the following alternative fragmentation sites: amino acids 38-40 (region 1); amino acids 100-102 (region 2); amino acids 113-117 (region 3); amino acids 152-156 (region 4); amino acids 167-171 (region 5); amino acids 182-184 (region 6). The positions of specific amino acid residues are shown for Glutamate 39 (E39), Aspartate 101 (D101), Aspartate 115 (D115), Glutamate 153 (E153), Aspartate 169 (D169), or Lysine 184 (K184).

The fragmentation sites relative to the nucleic acid sequence encoding the full-length mRFP1 polypeptide are depicted in Table 6.

**Table 4. Multiple alignment of coral (Anthozoa sp.) fluorescent proteins.** The numbering is based on A. victoria GFP (M.V. Matz et al., Nature Biotech. 17: 969-973, 1999). Two proteins from Zoanthus and two from Discosoma are compared pairwise. Introduced gaps are represented by dots. In the consensus sequences ("cns"), "O" marks an aromatic residue (Phe, Tyr, Trp, His); "@"=bulky hydrophobic residues (Val, Leu, Ile, Met, Phe, Trp); "+"=positively charged residues (His, Arg, Lys); "-"=negatively charged residues (Asp, Glu). "FP", fluorescent protein; 'z', Zoanthus; 'ds', Discosoma; 'dr', Discosoma 'red'; 'c', Clavularia; 'cns', consensus. DrFP583 is commonly referred to as 'DsRed' where 583 refers to the emission maximum at 583 nm (at an excitation maximum of 558 nm). By homology to the fragmentation sites chosen for GFP (Fig. 1A and 1B), alternative fragmentation sites of the coral fluorescent proteins which are the subject of the current invention are underlined.

	10	20	30	40	50	
MSKGEELFTG.VVPILVELDGDVNGHKFSVSGEGEDATY	<u>Y</u>	K	L	T	L	K
FTT.GKLPVP..W						

GFP (SEQ ID NO:2)



	MAQSKHGLTK.FMTMKYRMEGCVNKGKVFITGEGIGYPPKQKQAINLCVV..EGGPLPFAE	zFP506 (SEQ ID NO:9)
	MAHSHKGLKE.EMTMKYHMEGCVNKGKVFITGEGIGYPPKQKQAINLCVI..EGGPLPFSE	zFP538 (SEQ ID NO:10)
5	MSCSKSVIKE.EMLIDLHLEGTfNGHYFFIKGKGKQPNegTNTVTLVt KGGPLPFGW	dsFP483 (SEQ ID NO:11)
	MRSSKNVIKE.FMRFKVRMEGTvNGHEFFIEGEGEGRPYEGHNTVtKLKVT..KGGPLPFAW	drFP583 (SEQ ID NO:12)
10	MALSNKFIGD.DMKMTYHMDGCVNHYFTVKGEGNGKPYEGTQTSTFKVTMANGGPLAFSF	amFP486 (SEQ ID NO:13)
	KALTTMGVIKPDmKIKLMEGNVNGHAFVIEGEGEGKPYDGTHTLNLEVtKMAEGAPLPFSY	cFP484 (SEQ ID NO:14)
	MSKGEELFTG.VVPILVELDGDVNGHKFSVSGEGEGDATYgKLTtLKfICTT.GKLpVP..W	GFP
15	MAQSKHGLTK.FMTMKYRMEGCVNKGKVFITGEGIGYPPKQKQAINLCVV..EGGPLPFAE	zFP506
	MAHSHKGLKE.EMTMKYHMEGCVNKGKVFITGEGIGYPPKQKQAINLCVI..EGGPLPFSE	zFP538
20	MSCSKSVIKE.EMLIDLHLEGTfNGHYFFIKGKGKQPNegTNTVTLVt KGGPLPFGW	dsFP483
	MRSSKNVIKE.FMRFKVRMEGTvNGHEFFIEGEGEGRPYEGHNTVtKLKVT..KGGPLPFAW	drFP583
	MALSNKFIGD.DMKMTYHMDGCVNHYFTVKGEGNGKPYEGTQTSTFKVTMANGGPLAFSF	amFP486
	KALTTMGVIKPDmKIKLMEGNVNGHAFVIEGEGEGKPYDGTHTLNLEVtKMAEGAPLPFSY	cFP484
25	s M @ EG vnGH F @ GeG G Po G t@ @ V GgPLpF	cns. Anthozoa
	@ @ EG vnGH F @ GeG G G t@ @ P@p	cns. all
30	60 70 80 90 100 110	
	PTLVTTFSYGVQCFSRYPDHMKQHDFFKSAMPEGYVQERTIFFKLGNYKTRAEVKfEGD..	GFP
35	DILSAAFNYGNRVfTEYPQDIV..DYFKNSCPAGYTWDRSfLFEDGAVCICNADITVSVEN	zFP506
	DILSAGFKYGDRIFTEYPQDIV..DYFKNSCPAGYTWDRSfLFEDGAVCICNVDITVSVKEN	zFP538
40	HILCPQFQYGNKAFVHHPDNIH..DYLKLSFPEGYTWERSMHFEDGGLCCITNDISLTGN..	dsFP483
	DILSPQFQYGSKVYVKHPADIP..DYKLSFPEGFKWERVMNFEDGGVVTVTQDSSfQDG..	dsFP583
45	DILSTVFYKYNRCFTAYPTSMF..DYFKQAFPDGMSYERTFTYEDGGVATASWEISfLKN..	amFP486
	DILSNAFQYGNRALTKYPDDIA..DYFKQSFPEGYSWERTMTfELKGIVKVKSDISMEED..	cFP484
50	dILs F YGn+ f yP @ DYfK sfPeGo wER @ OEDg@ Dis@	cns. Anthozoa
	iL F YG f yP @ DyfK PeGo ER @ O D g De @	cns. all
55	120 130 140 150 160 170	
	TLVNRIELKGIDFKEDGNILGHKLEYNYNshNVYIMADKQNGIKVNFKIRHNIEDGfSVQL	GFP
60	CMYHESKFYGVNFPADGPVM.KKMTDNWEPSCeKIIPVfKQGIKGDVSMYLLfLKDGRRLR	zFP506
	CIYHKSIFNGMNFADGPVM.KKMTTNWEASCEKIMfVfKQGIKGDVSMYLLfLKDGRYR	zFP538
65	CFYyDIKFTGLNFPPNGPVV.QKKTtGWEPSTERLYP..RDEVLIGDIHhALTVEGfHYA	dsFP483
	CFIYKVKFfGVNFPDGPVM.QKKTtGWEASTERLYP..RDEVLKGEIHKALKfLKDGHYL	drFP583
70	CFEHKSTFHGVNFPADGPVM.AKKTtGWDPSFEKMTV..CDGfLKGdVTAFLMLQGGENYR	amFP486
	SFIYEIRFDGMNFPPNGPVV.QKKTtLWEPSTEIMYV..RDEVLVGDISHSLfLKGCHYR	cFP484
	c@ O f G@NfP dGPVm KkT WepS E+@ dG@L+GD@ L f GG+y	cns. Anthozoa
	@ @ G@Nf dG @@ K o @ @+ @ @G	cns. all
75	180 190 200 210 220 230	
	ADHYQQNTPIGDG.PVLLPDNHYLSTQSALS KDpNEKRdHMLLEFVTAAGIThGMDELYK	GFP
80	CQFDTVYKAKfSV..PRKMPDWHFIQHKLTREDRSdAKNQKWHLTeHAIASGSALP	zFP506
	CQFDTVYKAKfSV..PSKMPeWHFIQHKLLREDRSdAKNQKWLTeHAIAFPsALA	zFP538
85	CDIKTVYRAKfA..ALKMPGYHYVDTKLVIWNNDKEFM.KVEEHEIAVARHHPfYEPKDKD	dsFP483
	VEFKSIYMAKfA..PVQLPGYyyVDSKLDITSHNEDYT.IVEQYERTEGRHHLfL	drFP583
90	CQFHTSYKTKf..PVTMPPNHVEHRIARTDLdKGGN.SVQLTeHAVAHiTSVVPF	amFP486
	CDFKSIYKAKf..VVKLPDYHfVDHRIEILNHdKdYN.KVTLYENAVARYSLLPsQA	cFP484
95	c @ t@YkaKk pvk@P ho@Dh+@ @ l E a@a	cns. Anthozoa
	..... p @P ho@ @ l E a	cns. all

Table 5. Amino acid alignment of mRFP1 (SEQ ID NO:16) with A. victoria GFP (SEQ ID NO:2) showing alternative fragmentation sites (underlined) that are the subject of the present invention

# Aligned sequences: 2	
# 1: A. victoria GFP	
# 2: mRFP1	
# Matrix: EBLOSUM62	
# Gap penalty: 12	
# Extend penalty: 2	
#	
# Length: 240	
# Identity: 58/240 (24.2%)	
# Similarity: 109/240 (45.4%)	
# Gaps: 17/240 ( 7.1%)	
# Score: 186	
<pre>       10      20      30      40      50 GFP   MSKGEELFTGVVPILVELDGDVNGHKFSVSGEGEDA<u>NYG</u>KLTLKFICTT       ..... : : : : : mRFP1 MASSEDVIKEFMRFKVRMEGSVNGHEFEIEGEGEGRPY<u>EGT</u>QTAKLKVTK       10      20      30      40      50        60      70      80      90 GFP   G-KLPVPVPTLVTTFSYGVCFSRYPDHMKRHDFFKSAMPEGYVQERTIF       : mRFP1 GGPLPFAWDILSPQFQYGSKAYVKHPADIP--DYLKLSFPEGFKWERVMN       60      70      80      90  100    110    120    130    140 GFP   <u>FKDD</u>GNYKTRAEVKE<u>EGDT</u>LVNRIELKGIDFKEDGNILGHK-LEYNYNSH       : mRFP1 <u>FEDGG</u>VVTVTQDSS<u>LDGE</u>FIYKVKLRGTNFPDGPVMQKKTMGWEASTE 100    110    120    130    140  150    160    170    180    190 GFP   NVIYIMADKQKNGIKVNFKIRHNI<u>EDGS</u>VQLADHYQONTPI<u>G</u>DGPVLLPDN       : mRFP1 RMY---<u>PEDG</u>ALKGEIKMRLK<u>KLDG</u>GHYDAE--VKT<u>TYMA</u>KKPVLPGA 150    160    170    180    190  200    210    220    230 GFP   HYLSTQSAISKDPNEKRDHMLLEFVTAAGITHGMDELYK       : mRFP1 YKTDIKLDIT---SHNEDYTIVEQYERA----EGRHSTGA       200    210    220 </pre>	

Table 6. mRFP1 full length nucleic acid (SEQ ID NO:15) and amino acid sequence (SEQ ID NO:16). Alternative fragmentation sites that are the subject of the present invention are shown at the following regions (underlined): amino acids 38-40 (region 1); amino acids 100-102 (region 2); amino acids 152-156 (region 3); amino acids 167-171 (region 4); amino acids 182-191 (region 5). The positions of specific amino acid residues at the fragmentation sites for mRFP1 are shown for Glutamate 39 (E39), Aspartate 101 (D101), Aspartate 115 (D115), Glutamate 153 (E153), Aspartate 169 (D169), or Lysine 184 (K184).

10	atg gcc tcc tcc gag gac gtc atc aag gag ttc atg cgc ttc aag gtg cgc atg gag ggc	
	M A S S E D V I K E F M R F K V R M E G	
	1 5 10 15 20	
15	tcc gtg aac ggc cac gag ttc gag atc gag ggc gag ggc gag ggc cgc ccc <u>tac gag ggc</u>	
	S V N G H E F E I E G E G E G R P <u>Y E G</u>	
	21 25 30 35 40	E39 40
20	acc cag acc gcc aag ctg aag gtg acc aag ggc ggc ccc ctg ccc ttc gcc tgg gac atc T Q	
	T A K L K V T K G G P L P F A W D I	
	41 45 50 55 60	
25	ctg tcc cct cag ttc cag tac ggc tcc aag gcc tac gtg aag cac ccc gcc gac atc ccc	
	L S P Q F Q Y G S K A Y V K H P A D I P	
	61 65 70 75 80	
30	gac tac ttg aag ctg tcc ttc ccc gag ggc ttc aag tgg gag cgc gtg atg aac ttc <u>gag</u>	
	Y L K L S F P E G F K W E R V M N F <u>E</u>	
	81 85 90 95 100	D
35	<u>gag gag</u> ggc gtg gtg acc gtg acc cag gac tcc tcc <u>ctg cag gac ggc gag ttc atc tac</u>	
	<u>D G</u> G V V T V T Q D S S <u>L Q D G E</u> F I Y	
	D101 105 110 115 120	
40	aag gtg aag ctg cgc ggc acc aac ttc ccc tcc gac ggc ccc gta atg cag aag aag acc	
	V K L R G T N F P S D G P V M Q K K T	
	121 125 130 135 140	K
45	atg ggc tgg gag gcc tcc acc gag cgg atg tac <u>ccc gag gac ggc ggc</u> ctg aag ggc gag	
	M G W E A S T E R M Y <u>F E D G A</u> L K G E	
	141 145 150 155 160	E153
50	atc aag atg agg ctg aag <u>ctg aag gac ggc ggc</u> cac tac gac gcc gag gtc aag acc acc	
	I K M R L K <u>L K D G G</u> H Y D A E V K T T	
	161 165 170 175 180	D169
55	tac <u>atg gcc aag</u> aag ccc gtg cag ctg ccc ggc gcc tac aag acc gac atc aag ctg gac	
	Y <u>M A K</u> K P V Q L P G A Y K T D I K L D	
	181 185 190 195 200	K184
60	atc acc tcc cac aac gag gac tac acc atc gtg gaa cag tac gag cgc gcc gag ggc cgc I T	
	S H N E D Y T I V E Q Y E R A E G R	
	201 205 210 215 220	
65	cac tcc acc ggc gcc	
	H S T G A	
	221 225	

A PCA based on kindling fluorescent protein (KFP1) is also the subject of the present invention. In the case of KFP1, which is a variant of the fluorescent protein derived from *Anemonia sulcata*, the alternative fragmentation sites are based on the alignment of KFP1 to GFP as shown in Table 7. Table 8 shows the fragmentation sites relative to the full-length nucleotide and amino acid sequence of KFP1.

Table 7. Amino acid alignment of kindling fluorescent protein (KFP1)(SEQ ID NO:18) with A. victoria GFP(SEQ ID NO:2), showing alternative fragmentation sites(underlined) that are the subject of the present invention

5

```
#
# Aligned sequences: 2
# 1: A. victoria GFP
# 2: kindling fluorescent protein (KFP1)
# Matrix: EBLOSUM62
# Gap penalty: 12
# Extend penalty: 2
#
# Length: 241
# Identity:      57/241 (23.7%)
# Similarity:    98/241 (40.7%)
# Gaps:          12/241 ( 5.0%)
# Score: 145
```

---

	10	20	30	40
GFP	MSKGEELFTGVVPILVELDGDVNGHKFSVS	GE	GE	GDATY
KFP1	MAS---	LLTETMPFKTTIEGTVNGHC	FKCIGK	GEGNP
	10	20	30	40
	50	60	70	80
GFP	TGKLPVPWPPTLVTTFSYGVQCFSRYP	DHMKRHDFFKSAM	PEGYVQ	ERTIF
KFP1	GGPLPFAFHILSTSCMYGSKTFIKYV	S	GIP--	DYFKQSF
	50	60	70	80
	100	110	120	130
GFP	<u>FKDD</u> GNYKTRAEVKFE	GD	TLVNRIELK	GIDFKEDGNILGHKLEYN
KFP1	<u>YEDGG</u> FLTAHQDTS	LDG	DLVYKVKILGNNFPADGP	V
	100	110	120	130
	150	160	170	180
GFP	VYIMADKQ	ENG	IKVNF	KIRHN
KFP1	IVYEVDG	VL	RQSLMALKCPGGR	HLTCHLHTTYRSKKPAS
	150	160	170	180
	200	210	220	230
GFP	NHYLSTQS	ALSKDPNEKRDH	MVLL	EFVTAAGITHG
KFP1	DHRIEIM	EEVEKGKCYKQYEA	AVGRYCDAAPSKLG	----
	200	210	220	230

Table 8. Kindling fluorescent protein (KFP1) full length nucleic acid (SEQ ID NO:17) and amino acid sequence (SEQ ID NO:18). Alternative fragmentation sites that are the subject of the present invention are shown at the underlined regions: residues 35-37 (region 1); residues 97-99 (region 2); residues 110-114 (region 3); residues 150-156 (region 4); residues 167-171 (region 5); residues 184-195 (region 6). The positions of specific amino acid residues at the fragmentation sites for KFP1 are shown for Glutamate 36 (E36), Aspartate 98 (D98), Glycine 112 (G112), Valine 153 (V153), Histidine 169 (H169), or Alanine 186 (A186).

5	atg gcc tcc ctg ctg acc gag acc atg ccc ttc aag acc acc atc gag ggc acc gtg aac	
	M A S L L T E T M P F K T T I E G T V N	
	1 5 10 15 20	
15	ggc cac tgc ttc aag tgc atc ggc aag ggc gag ggc aac ccc ttc gag ggc acc cag gag	
	G H C F K C I G K G E G N P F E G T Q E	
	25 30 35 E36 40	
20	atg aag atc gag gtg atc gag ggc ggc ccc ctg ccc ttc gcc ttc cac atc ctg tcc acc	
	M K I E V I E G G P L P F A F H I L S T	
	45 50 55 60	
25	tcc tgc atg tac ggc tcc aag acc ttc atc aag tac gtg tcc ggc atc ccc gac tac ttc	
	S C M Y G S K T F I K Y V S G I P D Y F	
	65 70 75 80	
30	aag cag tcc ttc ccc gag ggc ttc acc tgg gag cgc acc acc acc tac gag gac ggc ggc	
	K Q S F P E G F T W E R T T T Y E D G G	
	85 90 95 D98 100	
35	ttc ctg acc gcc cac cag gac acc tcc ctg gac ggc gac tgc ctg gtg tac aag gtg aag	
	F L T A H Q D T S L D G D C L V Y K V K	
	105 110 G112 115 120	
40	atc ctg ggt aac aac ttc ccc gcc gac ggc ccc gtg atg cag aac aag gtc ggc cgc tgg	
	I L G N N F P A D G P V M Q N K V G R W	
	125 130 135 140	
45	gag ccc gga acc gag atc gtg tac gag gtg gac ggc gtg ctg cgc ggc cag tcc ctg atg	
	E P G T E I V Y E V D G V L R G Q S L M	
	145 150 V153 155 160	
50	gcc ctg aag tgc ccc ggc ggc cgg cac ctg acc tgc cac ctg cac acc acc tac cgc tcc	
	A L K C P G G R H L T C H L H T T Y R S	
	165 170 H169 175 180	
55	aag aag ccc gcc tcc gcc ctg aag atg ccc ggc ttc cac ttc gag gac cac cgc atc gag	
	K K P A S A L K M P G F H F E D H R I E	
	185 A186 190 195 200	
60	atc atg gag gag gtg gag aag ggc aag tgc tac aag cag tac gag gcc gcc gtg ggc cgc	
	I M E E V E K G K C Y K Q Y E A A V G R	
	205 210 215 220	
55	tac tgc gac gcc gcc ccc tcc aag ctg ggc cac aac	
	Y C D A A P S K L G H N	
	225 230	

It is a feature of PCA that the reassembled fragments are capable of re-creating the activity of the intact reporter from which the fragments are derived. For example, for a PCA based on dihydrofolate reductase (DHFR), the reassembled fragments are capable of binding

methotrexate in a manner similar to the full-length protein (I. Remy & S.W. Michnick, 1999, Proc Natl Acad Sci USA, 96: 5394-5399); in addition, mutations that affect the properties of the intact DHFR protein confer similar properties to the DHFR fragments when they are used in PCA (J.N. Pelletier, F.-X. C.-Valois & S.W. Michnick, 1998, Proc Natl Acad Sci USA 95: 12141-12146). Similarly, fragments of  $\beta$ -lactamase used in PCA are capable of cleavage of cephalosporin substrates with kinetics similar to the intact  $\beta$ -lactamase protein, and mutations that disrupt the molten globule structure of the intact protein improve the enzymatic properties of the reassembled fragments (A. Galarneau, M. Primeau, L.-E. Trudeau & S.W. Michnick, 2000, Nature Biotechnol. 20: 619-622).

Since the spectral properties of fluorescent proteins are critically dependent upon the orientation and proximity of amino acids relative to the core chromophore, it is not obvious that mutations that affect the spectral properties of an intact fluorescent protein would have the same effect when engineered into fragments of the protein. We reasoned that, if mutations that affect the spectral properties of fluorescent proteins could be engineered into protein-fragment complementation assays, it would be possible to generate a wide variety of PCAs with various spectral properties. Moreover, the availability of different color PCAs would enable the engineering of designer PCAs for a variety of applications in biology and biotechnology.

To demonstrate this principle, we created PCAs based on numerous variants of A. victoria green fluorescent protein and tested them by creating fusion constructs with several different human genes known to be involved in protein-protein interactions in mammalian cells. In the first example, fragments were generated for PCA by fragmenting an enhanced green fluorescent protein ("EGFP" in Table 3) in order to create a green fluorescent PCA (GFP PCA). The GFP fragments were then further mutated to create novel fragments having the mutations

S65G/V68L/S72A/T203Y which corresponds to the yellow fluorescent protein (YFP) variant named "10C" in Table 2, also referred to as enhanced yellow fluorescent protein ("EYFP") as in Table 3. With intact GFP, the introduction of the S65G/V68L/S72A/T203Y mutations into results in a protein with excitation and emission maxima at 514 nm and 527 nm, respectively, in which the chromophore matures fourfold faster than for the wild type GFP, generating a bright signal for cell biology applications. We sought to determine whether this GFP variant could be used in PCA and to assess the relative intensities of this YFP PCA versus the GFP PCA in cells transiently co-transfected with fragments fused to full-length proteins that had been previously reported to interact in human cells; this analysis is described in detail in Example 1, below.

To demonstrate the utility of the various fragment pairs that are the subject of the invention, we selected three of the fragmentation sites depicted in Fig. 1b and constructed PCAs based on YFP fragments fused to known interacting proteins in various gene/fragment orientations (NN, NC, CN and CC). In Example 2, described below, the results showed that the different fragmentation sites could in fact be used to construct alternative PCAs with good signals vs. background.

In two further examples of the engineering of PCAs based on mutant fragments, we further mutated the YFP fragments in order to determine if mutations shown to enhance the brightness of full-length YFP at physiological temperatures would confer similar properties when engineered into fragments for PCA. First, we engineered two additional mutations, S64L and M153T into YFP[1]. Both the S64L and M153T mutations improve the folding of full-length green fluorescent protein (Tsien, Ann. Rev. Biochem. ) and confer enhanced fluorescence to the intact, full-length protein (B .P. Cormack et al., Gene 173: 33-38). These mutations are a component of the YFP variant known as SEYFP (see Table 3). In example 3, described in detail

below, we directly compared a YFP PCA with the novel SEYFP PCA.

In yet another example of engineering mutant fragments for PCA, we introduced the mutation F46L into fragment 1 of SEYFP, generating novel fragment we designated IFP[1], and we introduced the mutations V163A and S175G into fragment 2 of YFP, generating novel  
5 fragment IFP[2]. These mutations are a component of the YFP variant known as SEYFP-F46L ('Venus') in Table 3. The results demonstrate the ability to engineer a highly intense fluorescent PCA (IFP PCA) by engineering mutant fragments of fluorescent proteins.

In a fourth example of the invention, we demonstrated the ability to create PCAs with specific desired spectral properties by creating mutant polypeptide fragments. We created a cyan  
10 fluorescent PCA (CFP PCA) by synthesizing fragments with mutations conferring a spectral shift to the blue region. This invention provides fragments for generating a wide spectrum of PCAs through genetic engineering including green, yellow, blue-green, blue, cyan, orange-red and red variants with various intensities and signal maturation characteristics.

In a final example of the invention, we demonstrated multi-color PCAs in which a single  
15 fragment of a fluorescent reporter generates different fluorescent colors within the same cell, depending upon the amino acid sequence of the fragment with which it is paired.

### Example 1

#### **20 Creation of fluorescent protein-fragment complementation assays and the generation of mutant fragments for PCA**

We sought to create two PCAs with different spectral properties starting with A. victoria GFP. First, GFP fragments were generated by PCR from a mammalian codon-optimized



version of GFP (pCMS-EGFP; Clontech). GFP[1] corresponded to amino acids 1 to 158 and GFP[2] to amino acids 159 to 239 of GFP. Second, fragments encoding a yellow variant of GFP (YFP PCA) were created by introducing the EYFP-specific mutations S65G, S72A into fragment 1 of GFP and the mutation T203Y into fragment 2 of GFP by PCR, resulting in fragments YFP[1] and YFP[2], respectively.

The fragments GFP[1], GFP[2], YFP[1], and YFP[2] were subcloned into a mammalian expression vector (pcDNA3.1Z, Invitrogen), which had previously been modified to incorporate the replication origin (oriP) of the Epstein Barr virus (EBV). The oriP allows episomal replication of these modified vectors in cell lines expressing the EBNA1 gene, such as HEK293E cells (293-EBNA, Invitrogen). Additionally, these vectors still retain the SV40 origin, allowing for episomal expression in cell lines expressing the SV40 large T antigen (e.g. HEK293T, Jurkat or COS) as well.

To test the activity and relative signal intensity of the GFP PCA versus the engineered YFP PCA, PCAs were created for three pairs of proteins that have previously been shown to interact in mammalian cells. These included the self-interaction of the tumor suppressor protein p53 (N.D. Lakin & S.P. Jackson, *Oncogene* 18: 7644-7655, 1999); the interaction of the papillomavirus E6 protein with p53 (B.A. Werness, A.J. Levine & P.M. Howley, *Science* 248: 76-79, 1990); and the interaction of the E6 protein with E6AP, a protein that mediates the interaction of E6 with p53 (J.M. Huibregtse, M. Scheffner & P.M. Howley, *Mol. Cell. Biol.* 13: 775-784, 1993). The full coding sequence for p53, E6 and E6AP was amplified by PCR from a sequence-verified full-length cDNA. The resulting PCR products were cleaned up by vacuum filtration (MultiScreen PCR, Amicon), digested with appropriate restriction enzymes to allow directional cloning, and fused in-frame to either the 5' or 3'-end of GFP[1], YFP[1], GFP[2] or

YFP[2] through a flexible linker encoding a 10-amino acid peptide (Gly.Gly.Gly.Gly.Ser)<sub>2</sub> (SEQ ID NO:19). The use of a flexible linker between the gene of interest and the reporter fragment assures that the orientation and arrangement of the fusions is optimal to bring the fluorescent protein fragments into close proximity (J.N. Pelletier, F.-X. C.-Valois & S.W. Michnick, 1998, 5 Proc Natl Acad Sci USA 95: 12141-12146). The orientations of the paired constructs was as follows: F1-linker-p53 with F2-linker-p53; F1-linker-E6 with E6AP-linker-F2; and F1-linker-E6 with F2-linker-p53, where F1 and F2 were the fragments of either GFP or YFP. DNAs from recombinant constructs were isolated using Qiagen Turbo BioRobot Prep kits (Qiagen, Chatsworth, CA) on a Beckman FX robotic workstation (Beckman Coulter, Fullerton, CA). 10 Isolated DNAs were quantitated and then normalized to a concentration of 50 ng/μl.

Twenty-four hours prior to transfection, HEK293E cells were plated (20,000 cells per well) in 24-well plates coated with poly-lysine, then co-transfected with 0.5 micrograms of DNA using Fugene transfection reagent (Roche Diagnostics, Indianapolis, IN), as per the manufacturer's recommendations. Following 24 hrs of expression, cells were washed once 15 with PBS and viewed on a Nikon TE-2000 microscope equipped with a HYQ-FITC filter cube (excitation: 460-500nm; emission:505-560 nm; dichroic mirror:505LP). Images were acquired with a CoolSnap HQ CCD camera. Figure 3 shows the results of fluorescence microscopy of GFP PCA vs. YFP PCA for the interactions of p53/p53, E6/E6AP and E6/p53. The reconstituted GFP or YFP signal could clearly be seen, and the subcellular localization of the complexes could 20 be determined consistent with their known localizations. However, the YFP PCA signal was visually brighter than the GFP PCA signal for all three protein-protein complexes, demonstrating that the YFP mutations previously shown to enhance the signal intensity of the full-length protein were also effective in enhancing the intensity of the reassembled fragments. Moreover,

the excitation and emission maxima of the YFP PCA were nearly identical to that of the intact fluorescent protein YFP 10c (Table 2), suggesting that the complementary fragments are capable of folding and generating a chromophore with substantially the same properties as that generated by the intact protein.

5

## **Example 2**

### **Alternative fragmentation sites in fluorescent proteins**

In order to demonstrate that fluorescent protein fragments generated from alternative fragmentation sites - that are the subject of the invention - could be used in PCA, fluorescent protein PCAs based were created for a yellow (YFP) fluorescent protein (see FIG. 4). cDNAs  
10 encoding full-length proteins (Pdk2, 14-3-3 $\sigma$ , and the components of the NF $\kappa$ B heterodimer p50 and p65) were fused to either the N- or C-terminus of complementary YFP fragments YFP[1] and YFP[2], corresponding to fragmentation of the full length protein at positions shown in FIG. 1a and FIG. 1b as Gln 157, Lys 158 or Asp 173, where the indicated amino acid residue  
15 represents the C-terminus of the N-terminal reporter fragment designated as YFP[1]. Formation of 14-3-3/14-3-3 dimers was used to assess the ability of each PCA fragment pair to allow for the detection of protein-protein complexes. Pdk2-YFP[1]/Pdk2-YFP[2] was used as a negative PCA control. HEK293E cells were transiently transfected with 100ng of each construct pair, and total fluorescence was evaluated 48 hrs later on a Molecular Devices Gemini XS platereader. Each bar  
20 represents the mean fluorescence of triplicate measurements, with error bars representing 95% confidence limits. Mock-transfected cells (no DNA or a single DNA construct) are shown in yellow. Various fragment orientations and combinations were tested, since optimal detection of complex formation may be orientation-dependent. In this example, the Lys158 and Asp173

fragmentation sites allowed detection of 14-3-3/14-3-3 complexes in all possible fragment combinations. The Gln156 fragmentation site allowed detection of 14-3-3/14-3-3 complexes in both the NC and CC orientations. Fragment/gene orientations were as follows: NN=14-3-3-YFP[1]/14-3-3-YFP[2]; NC=14-3-3-YFP[1]/YFP[2]-14-3-3; CN=YFP[1]-14-3-3/14-3-3-YFP[2]; CC=YFP[1]-14-3-3/YFP[2]-14-3-3). The results demonstrate the utility of the protein engineering principles that are incorporated into this invention, showing that various fragment pairs are useful for PCA. The compositions that are the subject of the invention include various fragment pairs incorporating a wide range of mutations useful for PCA.

### Example 3

#### **Mutant fragments generating a super-enhanced YFP PCA (SEYFP-PCA) and an intense fluorescent PCA (IFP PCA) with brighter signals than YFP PCA for biological applications**

To further demonstrate that the spectral properties of a PCA can be influenced by engineering mutant fragments, we first engineered the F64L and M153T mutations of SEYFP into YFP[1] by PCR, creating novel fragment SEYFP[1]. Subcloning was performed as described for Example 1. Fusion constructs were prepared as described above, for the interacting protein kinases MEK and ERK. Specific mutations in each reporter fragment confirmed by sequencing are noted, and are designated relative to wtGFP as in Table 2 and 3.

For quantitative measurements of fluorescence intensity, each well of a 96-well poly-lysine coated plate was seeded with 15,000 HEK293E cells 24 hours prior to transfection. Cells were transfected with 100 ng of DNA in total per well with FuGene transfection reagent, using conditions recommended by the manufacturer. The amount of each fusion construct varied from 50 ng of each construct to as little as 0.1 ng of each construct, with the remaining DNA supplied by an empty 'carrier' vector (e.g. up to 98 ng of carrier DNA for 2 ng total of fusion construct

DNA). All transfections were performed in triplicate. Twenty-four or forty-eight hours after transfection, the cells were stained with a 1:300 dilution of Hoescht 33342 (Molecular Probes, Eugene, OR) for 10 minutes, then washed several times with Dulbecco's phosphate buffered saline, then overlaid with a small volume of Hank's Buffered Salt Solution. After a 90 minute incubation at 37°C, mean fluorescence intensity data for each well were acquired on a SpectraMax Gemini XS Plate reader (Molecular Devices), using an excitation wavelength of 485 nm, emission of 527 nm and cutoff of 515 nm. For each sample PCA, mean fluorescence intensity was calculated from triplicate measurements. Relative fold increase in fluorescence was determined by normalizing the mean fluorescence intensity for the test PCA to that of the negative control.

As shown in FIG. 5, the MEK/ERK protein-protein complex could be detected with either of the two fluorescent PCAs. However, the use of SEYFP[1] ( F64L and M153T) instead of YFP[1] enhanced the signal intensity two-to four-fold. With this particular mutant YFP PCA (left side of histogram), signal could be readily detected over background with only 2 ng total of 'test' DNA. Moreover, 10 ng DNA for the YFP PCA (right side of histogram) gave a barely detectable signal, whereas the equivalent DNA for the SEYFP PCA gave a signal nearly four times background (left side of histogram). The example demonstrates that mutations known to enhance the intensity of the intact protein confer a similar property on the reassembled fragments.

Fig. 6 shows fluorescence microscopy images of the same PCAs as in Fig. 5, demonstrating that the additional mutations of SEYFP[1] (panel a) enhance the signal intensity as detected by fluorescence microscopy, enabling improved discrimination of the subcellular location of the protein-protein complexes. HEK293E cells were transfected with 5 ng of each

fusion construct (plus 90 ng carrier DNA). Images were acquired 48 hrs later using the Discovery-1 automated image acquisition system, using a 20 ms exposure time, and FITC filter set. Protein-protein complexes could also be readily visualized with the YFP PCA (panel b) but were less intense.

5            Since fragment 1 of these constructs contains all three of the amino acids that form the chromophore in the intact fluorescent protein, we also tested single mutant fragments YFP[1] and YFP[2] to ensure that individual fragments were incapable of generating a fluorescent signal. For panels c and d of Fig. 6, we transfected 50 ng of DNA from a single fusion construct with the indicated mutations. The left hand panel shows the fluorescence image; the right hand panel  
10 shows a DAPI stain of the cells, demonstrating that cells were present in the field that was imaged. Neither fragment alone, expressed as a fusion to protein Pdk2, gave a fluorescent signal. In subsequent analyses of over 6000 assays we found that under the experimental conditions we employed, the generation of a fluorescent PCA signal is dependent upon the interacting molecules. This is an important feature of the invention because it demonstrates that we are not  
15 tagging proteins with a fluorescent molecule. Rather, we are tagging proteins with polypeptide fragments which themselves are not fluorescent. The fluorescent signal is only generated upon interaction of the molecules to which the reporter fragments are fused. Interaction of the molecules of interest brings the reporter fragments into close proximity, allowing the fragments to fold together into an active structure capable of generating a fluorescent signal.

20            Figures 7a and 7b show the creation of yet another novel mutant fluorescent protein PCA allowing even greater sensitivity for biological applications. Mutations were selected based on the YFP variant designated SEYFP-F46L (Venus) in Table 3. These mutations have been shown to accelerate the maturation of the fluorescent signal in the intact protein (T. Nagai et al.,

2002, "A variant of yellow fluorescent protein with fast and efficient maturation for cell-biological applications", *Nature Biotech.* 20: 87-90). PCR mutagenesis was employed to incorporate the additional mutations F46L into SEYFP[1], and V163A and S175G into YFP[2], resulting in novel fragments we designated IFP[1] and IFP[2].

5            Formation of protein-protein complexes between the MAP kinase signaling proteins, MEK and ERK, was assessed with the novel IFP PCA by fusing MEK1 to the N-terminus of IFP[1] and ERK to the C-terminus of IFP[2]. As shown in FIGs. 7a and 7b, a titration series was performed wherein 100ng of total DNA was transfected per well, with the amount of DNA contributed by the PCA pair varying from 100ng down to 100pg, with the remaining DNA  
10   supplied by an empty 'carrier' vector. Fluorescence images were acquired 48 hours later on an SP Nikon fluorescence microscope using a HYQ-FITC filter cube (excitation: 460-500nm; emission:505-560 nm; dichroic mirror:505LP). Images were acquired with a CoolSnap HQ CCD camera with the indicated exposure times (in ms). Total fluorescence for each dilution of the MEK/ERK PCA was also quantified on a fluorescence platereader. Triplicate measurements  
15   for each dilution were made, and the mean fluorescence value was normalized to the mean fluorescence of a negative control PCA to determine the fold increase above the negative control, as shown in Figure 7b. Introduction of the additional mutations into the fragments of YFP greatly enhanced the fluorescent signal which could still be visualized (FIG. 7a) and quantified (FIG. 7b) even at 0.1 ng (100pg) of DNA. That level of DNA for the IFP PCA produced a  
20   significant signal above the negative control (1.5-fold increase). In contrast, to produce an equivalent fluorescence intensity with the YFP PCA, 10 ng DNA was needed.

The ability to identify the subcellular locations of protein-protein interactions enables high-content screening. For example, the trafficking of proteins within signaling pathways can

be seen. For example, we have used this approach with the IFP PCA described above to study the cytokine-induced translocation of the NF $\kappa$ B transcription complex of p65/p50 (FIG. 8). This protein-protein complex translocates from the cytoplasm to the nucleus in live cells in response to tumor necrosis factor. When p65 and p50 are tagged with complementary mutant fragments IFP[1] and IFP[2] respectively in transiently transfected cells, the fluorescent signal can be seen primarily in the cytoplasm in unstimulated cells 48 hours after transfection. Within 30 minutes of treatment of the TNF-responsive HEK cells with TNF-alpha, the fluorescent protein-protein complex moves predominantly to the nucleus.

The above examples demonstrate that mutations can be engineered into fluorescent protein fragments to confer specific desired properties for PCA. Accordingly, we have generated a number of novel fragments of fluorescent proteins incorporating previously described mutations of green fluorescent protein (see Table 2 and Table 3). These mutations have been engineered into fragments generated by fragmentation of fluorescent proteins at the sites depicted in Fig 1 and described in the above specification. Additionally, we have generated novel fragments at homologous fragmentation sites in coral fluorescent proteins (Table 4), in the monomeric red fluorescent protein (mRFP1) derived from DsRed (Table 5 and Table 6) and a kindling fluorescent protein (KFP1) derived from *Anemonia sulcata* (Table 7 and Table 8). The sequences of the novel fragments are shown in the Appendix prior to the claims of the present invention and are represented as SEQ ID NOS:20-1067 of the Sequence Listing and are the subject of the claimed invention. In general terms we refer to these as "mutant fragments". For the purposes of the invention, a "mutant fragment" is a fragment of a fluorescent protein that has one or more nucleotide or amino acid changes relative to the wild-type cDNA or protein.



## Example 4

### **Spectrally shifted PCAs**

Numerous examples of PCAs generating green fluorescent and yellow fluorescent signals have been described and demonstrated above. The invention described herein allows for PCAs generating a variety of spectral properties depending upon the amino acid sequence of the mutant fragments. In order to further demonstrate this principle, a PCA based on fragments of a cyan fluorescent protein was created to demonstrate blue fluorescence generated by a protein-protein interaction (FIG. 9). Two oligonucleotides corresponding to fragments of CFP were synthesized by Blue Heron Biotechnology (Bothell, WA). The resulting fragments were amplified by PCR to attach restriction sites and a flexible 10-aa linker for cloning into a pcDNA3-based expression vector, resulting in vectors containing CFP[1] (encoding aa 1-158 of ECFP) or CFP[2] (encoding aa 159-239 of ECFP) where the CFP had the amino acid sequence shown as ECFP in Table 3. The proteins Pdk2 and 14-3-3 $\sigma$  were fused to the N-terminus of CFP[1] and CFP[2], respectively, while the subunits of the NF $\kappa$ B heterodimer p50 and p65 were fused to the C-terminus of the CFP fragments. The construct pairs 14-3-3 $\sigma$ /14-3-3 $\sigma$ , p65/p50 and the Pdk2/Pdk2 negative control were transiently transfected into HEK293T cells, and fluorescence microscopy was performed after 48 hours. Fluorescence images were acquired on an SP Nikon fluorescence microscope using a Chroma CFP filter (excitation: 426-446nm; emission:460-500nm; dichroic mirror:455LP). Images were acquired with a CoolSnap HQ CCD camera with exposure times of 1-5 sec, as shown in Figure 8. The results show that mutations causing a spectral shift in the intact fluorescent protein can be engineered into fragments for PCA, resulting in a PCA generating a blue fluorescent signal with utility for biological applications.

## Example 5

### **Multi-color PCAs**

The availability of a suite of fluorescent protein PCAs enables the construction of multi-  
5 color PCAs for a variety of biology, biotechnology, drug discovery and diagnostic applications.  
Such multi-color PCAs are another aspect of the invention.

For example, a 'generic' F2 polypeptide fragment could be combined with multiple  
distinct F1 mutant fragments in order to detect two, three, four or more bimolecular events  
simultaneously. This can be achieved by fragmenting a fluorescent protein in such a way that F1  
10 contains all the amino acid residues necessary for chromophore formation when complemented  
by F2. Two or more mutant fragments of F1 are then created. For example, mutant F1  
fragments that are capable of reconstituting either a green, yellow, cyan, blue or red signal can be  
generated. If F2 is fused to molecule A, and the mutant F1 fragments are fused separately to  
molecules B, C, D, E and F respectively, the interactions of A with B, A with C, A with D, A  
15 with E and A with F can all be tested simultaneously by testing for a fluorescence signal at the 5  
different wavelengths that are generated by fragment complementation.

We demonstrated the principles of multi-color PCA in living cells by using the ability of  
the NF $\kappa$ B p65 subunit to form complexes with the p50 subunit, and also with the protein I $\kappa$ B $\alpha$ ,  
as a model system. In resting cells, I $\kappa$ B $\alpha$  binds to NF $\kappa$ B and retains the complex in the  
20 cytoplasm. Thus, p65 forms cytoplasmic protein-protein complexes with p50 and also with  
I $\kappa$ B $\alpha$ . We co- transfected HEK293T cells simultaneously with three PCA constructs: CFP[1]-  
p50 ; CFP[2]-p65; and I $\kappa$ B $\alpha$  -YFP[1]. Fluorescence images were acquired with an SP Nikon  
fluorescence microscope using a Chroma CFP filter (excitation: 426-446nm; emission:460-

500nm; dichroic mirror:455LP), and a FITC filter (excitation: 460-500nm; emission:505-560 nm; dichroic mirror:505LP). 16-bit monochrome images were acquired with a CoolSnap HQ CCD camera. CFP and FITC images for each PCA were subsequently pseudocolored and overlaid using Metamorph software (Molecular Devices). If a protein-protein complex forms between p50 and p65, the CFP[1] fragment should complement the CFP[2] fragment, producing blue fluorescence. Alternatively, if a protein-protein complex forms between I $\kappa$ B $\alpha$  and p65, the YFP[1] fragment should complement the CFP[2] fragment, producing a yellow fluorescence. As shown in FIG. 10, both p65/p50 (blue) and I $\kappa$ B $\alpha$ /p65 (yellow) complexes could be detected in the cytoplasm as expected. Cells displaying a lighter yellow (almost white) cytoplasmic staining pattern are expressing both p65/p50 and I $\kappa$ B $\alpha$ /p65 complexes. The ability to construct multi-color PCAs allows for the detection and quantification of multiple distinct protein-protein complexes within the same cells.

### **Additional Applications of Fluorescent Protein PCAs**

The many practical applications of this invention include high-content and high-throughput assays in living cells, cell lysates, or in vitro formats. The applications of the invention include the detection of pathway activation and pathway 'switching' in living cells by agonists, antagonists and inhibitors. The translocation or trafficking of proteins from one subcellular compartment to another can be followed; if protein A initially binds to protein B at the cell membrane and generates a yellow fluorescent signal, and then moves to the cell nucleus and binds to protein C and generates a cyan fluorescent signal, the ratio of cyan to yellow can be used as a detector of the activation of the translocation event. Moreover, there are many applications for fluorescent protein PCAs in diagnostics and nanotechnology. For example,

mutant F1 fragments could be bound to a solid surface array, each one as a fusion with a different antibody, which could be used to detect the presence of specific antigens in a sample. The applications of multicolor PCAs include rapid, multicolor diagnostics for biowarfare agents. Such multicolor PCAs are made possible by the novel mutant fragments that are the subject of  
5 the present invention.

The cells can be studied in vitro in a variety of formats including tissue culture plates, microtiter plates, or slide formats. The cells harboring PCA constructs can also be studied in vivo. For example, suitable cultured cells stably expressing a particular PCA can be grown as ascites in living animals, or introduced into nude mice to form tumors. Alternative, transgenic  
10 mice harboring the PCA constructs can be made. The protein-protein complexes within the animal can then be studied by whole animal imaging systems, for example, those supplied by Xenogen (Alameda, CA) or Anti-Cancer (San Diego, CA). All the PCAs presented here, and the various intense yellow and red fluorescent PCAs, will be particularly useful for PCA in vivo. In vivo PCA applications include the ability to generate a PCA that responds in vivo to the  
15 consumption or injection of a drug by the animal. Applications to pre-clinical drug development include the ability to perform ADME studies (absorption, distribution, metabolism or excretion of a drug) in live animals without sampling blood or urine. For example, if a drug causes an increase or decrease in a specific protein-protein complex within a cell in the live animal, the fluorescent signal can be acquired at various times after drug administration which will allow  
20 estimation of the pharmacokinetic and pharmacodynamic properties of the drug in whole animals.

Finally, the availability of a wide range of complementing mutant fragments of fluorescent proteins enables empirical testing for mutant fragment combinations that are

particularly useful for PCA. It is likely that this combinatorial feature of PCA will enable the generation of a large number of novel assays with a range of colors, intensities, combinations and physical properties for use in drug screening, target validation, ADME, and diagnostics applications.

5

The entire contents including the references cited therein of the following patents and publications are incorporated by reference in their entirety for all purposes to the same extent as if each individual patent, patent application or publication were so individually denoted.

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10	6,294,330	Michnick, et al.
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The sequences of the novel fragments are shown in the Appendix below and are represented as SEQ ID NOS:20-1067 of the Sequence Listing and are the subject of the claimed  
10 invention.

# APPENDIX

GFPF1 (aa 1-39 of wt GFP) pos. 1 Met removed	
5	SEQ ID NOS:20 & 21
	<div> <div> <div>agt</div> <div>aaa</div> <div>gga</div> <div>gaa</div> <div>gaa</div> <div>ctt</div> <div>ttc</div> <div>act</div> <div>gga</div> <div>gtt</div> <div>gtc</div> <div>cca</div> <div>att</div> <div>ctt</div> <div>gtt</div> <div>gaa</div> </div> <div>48</div> </div> <div> <div>Ser</div> <div>Lys</div> <div>Gly</div> <div>Glu</div> <div>Glu</div> <div>Leu</div> <div>Phe</div> <div>Thr</div> <div>Gly</div> <div>Val</div> <div>Val</div> <div>Pro</div> <div>Ile</div> <div>Leu</div> <div>Val</div> <div>Glu</div> </div> <div> <div>1</div> <div>5</div> <div>10</div> <div>15</div> </div>



	caa caa aat act cca att ggc gat ggc cct gtc ctt tta cca gac aac	480
	Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn	
	145 150 155 160	
5	cat tac ctg tcc aca caa tct gcc ctt tcg aaa gat ccc aac gaa aag	528
	His Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys	
	165 170 175	
10	aga gac cac atg gtc ctt ctt gag ttt gta aca gct gct ggg att aca	576
	Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr	
	180 185 190	
15	cat ggc atg gat gaa cta tac aaa	600
	His Gly Met Asp Glu Leu Tyr Lys	
	195 200	
20	YFPF1A (aa 1-40 of EYFP) - Met @ position 1	
	SEQ ID NOS:24 & 25	
	gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc	48
	Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val	
	1 5 10 15	
25	gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag	96
	Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu	
	20 25 30	
30	ggc gag ggc gat gcc acc tac	117
	Gly Glu Gly Asp Ala Thr Tyr	
	35	
35	YFPF2A (aa 41-239 of EYFP) + Met @ position 1	
	SEQ ID NOS:26 & 27	
40	atg ggc aag ctg acc ctg aag ttc atc tgc acc acc ggc aag ctg ccc	48
	Met Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro	
	1 5 10 15	
45	gtg ccc tgg ccc acc ctc gtg acc acc ttc ggc tac ggc ctg cag tgc	96
	Val Pro Trp Pro Thr Leu Val Thr Thr Phe Gly Tyr Gly Leu Gln Cys	
	20 25 30	
50	ttc gcc cgc tac ccc gac cac atg aag cgg cac gac ttc ttc aag tcc	144
	Phe Ala Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser	
	35 40 45	
55	gcc atg ccc gaa ggc tac gtc cag gag cgc acc atc ttc ttc aag gac	192
	Ala Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp	
	50 55 60	
60	gac ggc aac tac aag acc cgc gcc gag gtg aag ttc gag ggc gac acc	240
	Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr	
	65 70 75 80	

	ctg gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag gac ggc	288
	Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly	
	85 90 95	
5	aac atc ctg ggg cac aag ctg gag tac aac tac aac agc cac aac gtc	336
	Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val	
	100 105 110	
10	tat atc atg gcc gac aag cag aag aac ggc atc aag gtg aac ttc aag	384
	Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys	
	115 120 125	
15	atc cgc cac aac atc gag gac ggc agc gtg cag ctc gcc gac cac tac	432
	Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr	
	130 135 140	
20	cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc gac aac	480
	Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn	
	145 150 155 160	
25	cac tac ctg agc tac cag tcc gcc ctg agc aaa gac ccc aac gag aag	528
	His Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys	
	165 170 175	
30	cgc gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg atc act	576
	Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr	
	180 185 190	
35	ctc ggc atg gac gag ctg tac aag	600
	Leu Gly Met Asp Glu Leu Tyr Lys	
	195 200	
35	YFPF2A F46L mutation	
	SEQ ID NOS:28 & 29	
40	ggc aag ctg acc ctg aag ctg atc tgc acc acc ggc aag ctg ccc gtg	48
	Gly Lys Leu Thr Leu Lys Leu Ile Cys Thr Thr Gly Lys Leu Pro Val	
	1 5 10 15	
45	ccc tgg ccc acc ctc gtg acc acc ttc ggc tac ggc ctg cag tgc ttc	96
	Pro Trp Pro Thr Leu Val Thr Thr Phe Gly Tyr Gly Leu Gln Cys Phe	
	20 25 30	
50	gcc cgc tac ccc gac cac atg aag cgg cac gac ttc ttc aag tcc gcc	144
	Ala Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser Ala	
	35 40 45	
55	atg ccc gaa ggc tac gtc cag gag cgc acc atc ttc ttc aag gac gac	192
	Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp	
	50 55 60	
60	ggc aac tac aag acc cgc gcc gag gtg aag ttc gag ggc gac acc ctg	240
	Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu	
	65 70 75 80	

	gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag gac ggc aac	288
	Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn	
	85 90 95	
5	atc ctg ggg cac aag ctg gag tac aac tac aac agc cac aac gtc tat	336
	Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr	
	100 105 110	
10	atc atg gcc gac aag cag aag aac ggc atc aag gtg aac ttc aag atc	384
	Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile	
	115 120 125	
15	cgc cac aac atc gag gac ggc agc gtg cag ctc gcc gac cac tac cag	432
	Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln	
	130 135 140	
20	cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc gac aac cac	480
	Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His	
	145 150 155 160	
	tac ctg agc tac cag tcc gcc ctg agc aaa gac ccc aac gag aag cgc	528
	Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg	
	165 170 175	
25	gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg atc act ctc	576
	Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr Leu	
	180 185 190	
30	ggc atg gac gag ctg tac aag	597
	Gly Met Asp Glu Leu Tyr Lys	
	195	
35	YFPF2A F46L mutation + Met @ postion 1	
	SEQ ID NOS:30 & 31	
40	atg ggc aag ctg acc ctg aag ctg atc tgc acc acc ggc aag ctg ccc	48
	Met Gly Lys Leu Thr Leu Lys Leu Ile Cys Thr Thr Gly Lys Leu Pro	
	1 5 10 15	
	gtg ccc tgg ccc acc ctc gtg acc acc ttc ggc tac ggc ctg cag tgc	96
	Val Pro Trp Pro Thr Leu Val Thr Thr Phe Gly Tyr Gly Leu Gln Cys	
	20 25 30	
45	ttc gcc cgc tac ccc gac cac atg aag cgg cac gac ttc ttc aag tcc	144
	Phe Ala Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser	
	35 40 45	
50	gcc atg ccc gaa ggc tac gtc cag gag cgc acc atc ttc ttc aag gac	192
	Ala Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp	
	50 55 60	
55	gac ggc aac tac aag acc cgc gcc gag gtg aag ttc gag ggc gac acc	240
	Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr	
	65 70 75 80	

	ctg gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag gac ggc	288
	Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly	
	85 90 95	
5	aac atc ctg ggg cac aag ctg gag tac aac tac aac agc cac aac gtc	336
	Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val	
	100 105 110	
10	tat atc atg gcc gac aag cag aag aac ggc atc aag gtg aac ttc aag	384
	Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys	
	115 120 125	
15	atc cgc cac aac atc gag gac ggc agc gtg cag ctc gcc gac cac tac	432
	Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr	
	130 135 140	
20	cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc gac aac	480
	Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn	
	145 150 155 160	
	cac tac ctg agc tac cag tcc gcc ctg agc aaa gac ccc aac gag aag	528
	His Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys	
	165 170 175	
25	cgc gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg atc act	576
	Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr	
	180 185 190	
30	ctc ggc atg gac gag ctg tac aag	600
	Leu Gly Met Asp Glu Leu Tyr Lys	
	195 200	
35	YFPF2A F46L/F64L mutations	
	SEQ ID NOS:32 & 33	
40	ggc aag ctg acc ctg aag ctg atc tgc acc acc ggc aag ctg ccc gtg	48
	Gly Lys Leu Thr Leu Lys Leu Ile Cys Thr Thr Gly Lys Leu Pro Val	
	1 5 10 15	
	ccc tgg ccc acc ctc gtg acc acc ctg ggc tac ggc ctg cag tgc ttc	96
	Pro Trp Pro Thr Leu Val Thr Thr Leu Gly Tyr Gly Leu Gln Cys Phe	
	20 25 30	
45	gcc cgc tac ccc gac cac atg aag cgg cac gac ttc ttc aag tcc gcc	144
	Ala Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser Ala	
	35 40 45	
50	atg ccc gaa ggc tac gtc cag gag cgc acc atc ttc ttc aag gac gac	192
	Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp	
	50 55 60	
55	ggc aac tac aag acc cgc gcc gag gtg aag ttc gag ggc gac acc ctg	240
	Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu	
	65 70 75 80	

	gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag gac ggc aac	288
	Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn	
	85 90 95	
5	atc ctg ggg cac aag ctg gag tac aac tac aac agc cac aac gtc tat	336
	Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr	
	100 105 110	
10	atc atg gcc gac aag cag aag aac ggc atc aag gtg aac ttc aag atc	384
	Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile	
	115 120 125	
15	cgc cac aac atc gag gac ggc agc gtg cag ctc gcc gac cac tac cag	432
	Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln	
	130 135 140	
20	cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc gac aac cac	480
	Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His	
	145 150 155 160	
25	tac ctg agc tac cag tcc gcc ctg agc aaa gac ccc aac gag aag cgc	528
	Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg	
	165 170 175	
30	gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg atc act ctc	576
	Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr Leu	
	180 185 190	
35	ggc atg gac gag ctg tac aag	597
	Gly Met Asp Glu Leu Tyr Lys	
	195	
35	YFPF2A F46L/F64L mutations + Met @ posit. 1	
	SEQ ID NOS:34 & 35	
40	atg ggc aag ctg acc ctg aag ctg atc tgc acc acc ggc aag ctg ccc	48
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	1 5 10 15	
45	gtg ccc tgg ccc acc ctc gtg acc acc ctg ggc tac ggc ctg cag tgc	96
	Val Pro Trp Pro Thr Leu Val Thr Thr Leu Gly Tyr Gly Leu Gln Cys	
	20 25 30	
50	ttc gcc cgc tac ccc gac cac atg aag cgg cac gac ttc ttc aag tcc	144
	Phe Ala Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser	
	35 40 45	
55	gcc atg ccc gaa ggc tac gtc cag gag cgc acc atc ttc ttc aag gac	192
	Ala Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp	
	50 55 60	
60	gac ggc aac tac aag acc cgc gcc gag gtg aag ttc gag ggc gac acc	240
	Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr	
	65 70 75 80	

	ctg gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag gac ggc	288
	Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly	
	85 90 95	
5	aac atc ctg ggg cac aag ctg gag tac aac tac aac agc cac aac gtc	336
	Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val	
	100 105 110	
10	tat atc atg gcc gac aag cag aag aac ggc atc aag gtg aac ttc aag	384
	Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys	
	115 120 125	
15	atc cgc cac aac atc gag gac ggc agc gtg cag ctc gcc gac cac tac	432
	Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr	
	130 135 140	
20	cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc gac aac	480
	Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn	
	145 150 155 160	
25	cac tac ctg agc tac cag tcc gcc ctg agc aaa gac ccc aac gag aag	528
	His Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys	
	165 170 175	
30	ctc ggc atg gac gag ctg tac aag	600
	Leu Gly Met Asp Glu Leu Tyr Lys	
	195 200	
35	YFPF2A F64L mutation	
	SEQ ID NOS:36 & 37	
40	ggc aag ctg acc ctg aag ttc atc tgc acc acc ggc aag ctg ccc gtg	48
	Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val	
	1 5 10 15	
45	ccc tgg ccc acc ctc gtg acc acc ctg ggc tac ggc ctg cag tgc ttc	96
	Pro Trp Pro Thr Leu Val Thr Thr Leu Gly Tyr Gly Leu Gln Cys Phe	
	20 25 30	
50	gcc cgc tac ccc gac cac atg aag cgg cac gac ttc ttc aag tcc gcc	144
	Ala Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser Ala	
	35 40 45	
55	atg ccc gaa ggc tac gtc cag gag cgc acc atc ttc ttc aag gac gac	192
	Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp	
	50 55 60	
60	ggc aac tac aag acc cgc gcc gag gtg aag ttc gag ggc gac acc ctg	240
	Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu	
	65 70 75 80	

	gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag gac ggc aac	288
	Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn	
	85 90 95	
5	atc ctg ggg cac aag ctg gag tac aac tac aac agc cac aac gtc tat	336
	Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr	
	100 105 110	
10	atc atg gcc gac aag cag aag aac ggc atc aag gtg aac ttc aag atc	384
	Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile	
	115 120 125	
15	cgc cac aac atc gag gac ggc agc gtg cag ctc gcc gac cac tac cag	432
	Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln	
	130 135 140	
20	cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc gac aac cac	480
	Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His	
	145 150 155 160	
	tac ctg agc tac cag tcc gcc ctg agc aaa gac ccc aac gag aag cgc	528
	Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg	
	165 170 175	
25	gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg atc act ctc	576
	Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr Leu	
	180 185 190	
30	ggc atg gac gag ctg tac aag	597
	Gly Met Asp Glu Leu Tyr Lys	
	195	
35	YFPF2A F64L mutation + Met @ position 1	
	SEQ ID NOS:38 & 39	
40	atg ggc aag ctg acc ctg aag ttc atc tgc acc acc ggc aag ctg ccc	48
	Met Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro	
	1 5 10 15	
	gtg ccc tgg ccc acc ctc gtg acc acc ctg ggc tac ggc ctg cag tgc	96
	Val Pro Trp Pro Thr Leu Val Thr Thr Leu Gly Tyr Gly Leu Gln Cys	
	20 25 30	
45	ttc gcc cgc tac ccc gac cac atg aag cgg cac gac ttc ttc aag tcc	144
	Phe Ala Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser	
	35 40 45	
50	gcc atg ccc gaa ggc tac gtc cag gag cgc acc atc ttc ttc aag gac	192
	Ala Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp	
	50 55 60	
55	gac ggc aac tac aag acc cgc gcc gag gtg aag ttc gag ggc gac acc	240
	Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr	
	65 70 75 80	

	ctg gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag gac ggc	288
	Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly	
	85 90 95	
5	aac atc ctg ggg cac aag ctg gag tac aac tac aac agc cac aac gtc	336
	Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val	
	100 105 110	
10	tat atc atg gcc gac aag cag aag aac ggc atc aag gtg aac ttc aag	384
	Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys	
	115 120 125	
15	atc cgc cac aac atc gag gac ggc agc gtg cag ctc gcc gac cac tac	432
	Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr	
	130 135 140	
20	cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc gac aac	480
	Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn	
	145 150 155 160	
	cac tac ctg agc tac cag tcc gcc ctg agc aaa gac ccc aac gag aag	528
	His Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys	
	165 170 175	
25	cgc gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg atc act	576
	Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr	
	180 185 190	
30	ctc ggc atg gac gag ctg tac aag	600
	Leu Gly Met Asp Glu Leu Tyr Lys	
	195 200	
35	YFPF2A K79R mutation	
	SEQ ID NOS:40 & 41	
40	ggc aag ctg acc ctg aag ttc atc tgc acc acc ggc aag ctg ccc gtg	48
	Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val	
	1 5 10 15	
	ccc tgg ccc acc ctc gtg acc acc ttc ggc tac ggc ctg cag tgc ttc	96
	Pro Trp Pro Thr Leu Val Thr Thr Phe Gly Tyr Gly Leu Gln Cys Phe	
	20 25 30	
45	gcc cgc tac ccc gac cac atg cgc cgg cac gac ttc ttc aag tcc gcc	144
	Ala Arg Tyr Pro Asp His Met Arg Arg His Asp Phe Phe Lys Ser Ala	
	35 40 45	
50	atg ccc gaa ggc tac gtc cag gag cgc acc atc ttc ttc aag gac gac	192
	Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp	
	50 55 60	
55	ggc aac tac aag acc cgc gcc gag gtg aag ttc gag ggc gac acc ctg	240
	Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu	
	65 70 75 80	



	gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag gac ggc aac	288
	Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn	
	85 90 95	
5	atc ctg ggg cac aag ctg gag tac aac tac aac agc cac aac gtc tat	336
	Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr	
	100 105 110	
10	atc atg gcc gac aag cag aag aac ggc atc aag gtg aac ttc aag atc	384
	Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile	
	115 120 125	
15	cgc cac aac atc gag gac ggc agc gtg cag ctc gcc gac cac tac cag	432
	Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln	
	130 135 140	
20	cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc gac aac cac	480
	Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His	
	145 150 155 160	
	tac ctg agc tac cag tcc gcc ctg agc aaa gac ccc aac gag aag cgc	528
	Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg	
	165 170 175	
25	gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg atc act ctc	576
	Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr Leu	
	180 185 190	
30	ggc atg gac gag ctg tac aag	597
	Gly Met Asp Glu Leu Tyr Lys	
	195	
35	YFPF2A K79R mutation + Met @ posit. 1	
	SEQ ID NOS:42 & 43	
40	atg ggc aag ctg acc ctg aag ttc atc tgc acc acc ggc aag ctg ccc	48
	Met Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro	
	1 5 10 15	
	gtg ccc tgg ccc acc ctc gtg acc acc ttc ggc tac ggc ctg cag tgc	96
	Val Pro Trp Pro Thr Leu Val Thr Thr Phe Gly Tyr Gly Leu Gln Cys	
	20 25 30	
45	ttc gcc cgc tac ccc gac cac atg cgc cgg cac gac ttc ttc aag tcc	144
	Phe Ala Arg Tyr Pro Asp His Met Arg Arg His Asp Phe Phe Lys Ser	
	35 40 45	
50	gcc atg ccc gaa ggc tac gtc cag gag cgc acc atc ttc ttc aag gac	192
	Ala Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp	
	50 55 60	
55	gac ggc aac tac aag acc cgc gcc gag gtg aag ttc gag ggc gac acc	240
	Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr	
	65 70 75 80	

	ctg gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag gac ggc	288
	Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly	
	85 90 95	
5	aac atc ctg ggg cac aag ctg gag tac aac tac aac agc cac aac gtc	336
	Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val	
	100 105 110	
10	tat atc atg gcc gac aag cag aag aac ggc atc aag gtg aac ttc aag	384
	Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys	
	115 120 125	
15	atc cgc cac aac atc gag gac ggc agc gtg cag ctc gcc gac cac tac	432
	Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr	
	130 135 140	
20	cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc gac aac	480
	Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn	
	145 150 155 160	
	cac tac ctg agc tac cag tcc gcc ctg agc aaa gac ccc aac gag aag	528
	His Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys	
	165 170 175	
25	cgc gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg atc act	576
	Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr	
	180 185 190	
30	ctc ggc atg gac gag ctg tac aag	600
	Leu Gly Met Asp Glu Leu Tyr Lys	
	195 200	
35	YFPF2A Y66F mutation	
	SEQ ID NOS:44 & 45	
40	ggc aag ctg acc ctg aag ttc atc tgc acc acc ggc aag ctg ccc gtg	48
	Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val	
	1 5 10 15	
45	ccc tgg ccc acc ctc gtg acc acc ttc ggc ttc ggc ctg cag tgc ttc	96
	Pro Trp Pro Thr Leu Val Thr Thr Phe Gly Phe Gly Leu Gln Cys Phe	
	20 25 30	
	ggc cgc tac ccc gac cac atg aag cgg cac gac ttc ttc aag tcc gcc	144
	Ala Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser Ala	
	35 40 45	
50	atg ccc gaa ggc tac gtc cag gag cgc acc atc ttc ttc aag gac gac	192
	Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp	
	50 55 60	
55	ggc aac tac aag acc cgc gcc gag gtg aag ttc gag ggc gac acc ctg	240
	Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu	
	65 70 75 80	

	gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag gac ggc aac	288
	Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn	
	85 90 95	
5	atc ctg ggg cac aag ctg gag tac aac tac aac agc cac aac gtc tat	336
	Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr	
	100 105 110	
10	atc atg gcc gac aag cag aag aac ggc atc aag gtg aac ttc aag atc	384
	Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile	
	115 120 125	
15	cgc cac aac atc gag gac ggc agc gtg cag ctc gcc gac cac tac cag	432
	Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln	
	130 135 140	
20	cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc gac aac cac	480
	Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His	
	145 150 155 160	
25	tac ctg agc tac cag tcc gcc ctg agc aaa gac ccc aac gag aag cgc	528
	Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg	
	165 170 175	
30	gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg atc act ctc	576
	Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr Leu	
	180 185 190	
35	ggc atg gac gag ctg tac aag	597
	Gly Met Asp Glu Leu Tyr Lys	
	195	
40	YFPF2A Y66F mutation + Met @ posit. 1	
	SEQ ID NOS:46 & 47	
40	atg ggc aag ctg acc ctg aag ttc atc tgc acc acc ggc aag ctg ccc	48
	Met Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro	
	1 5 10 15	
45	gtg ccc tgg ccc acc ctc gtg acc acc ttc ggc ttc ggc ctg cag tgc	96
	Val Pro Trp Pro Thr Leu Val Thr Thr Phe Gly Phe Gly Leu Gln Cys	
	20 25 30	
50	ttc gcc cgc tac ccc gac cac atg aag cgg cac gac ttc ttc aag tcc	144
	Phe Ala Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser	
	35 40 45	
55	gcc atg ccc gaa ggc tac gtc cag gag cgc acc atc ttc ttc aag gac	192
	Ala Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp	
	50 55 60	
60	gac ggc aac tac aag acc cgc gcc gag gtg aag ttc gag ggc gac acc	240
	Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr	
	65 70 75 80	

	ctg gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag gac ggc	288
	Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly	
	85 90 95	
5	aac atc ctg ggg cac aag ctg gag tac aac tac aac agc cac aac gtc	336
	Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val	
	100 105 110	
10	tat atc atg gcc gac aag cag aag aac ggc atc aag gtg aac ttc aag	384
	Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys	
	115 120 125	
15	atc cgc cac aac atc gag gac ggc agc gtg cag ctc gcc gac cac tac	432
	Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr	
	130 135 140	
20	cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc gac aac	480
	Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn	
	145 150 155 160	
	cac tac ctg agc tac cag tcc gcc ctg agc aaa gac ccc aac gag aag	528
	His Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys	
	165 170 175	
25	cgc gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg atc act	576
	Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr	
	180 185 190	
30	ctc ggc atg gac gag ctg tac aag	600
	Leu Gly Met Asp Glu Leu Tyr Lys	
	195 200	
35	YFPF2A Q69K mutation	
	SEQ ID NOS:48 & 49	
40	ggc aag ctg acc ctg aag ttc atc tgc acc acc ggc aag ctg ccc gtg	48
	Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val	
	1 5 10 15	
	ccc tgg ccc acc ctc gtg acc acc ttc ggc tac ggc ctg aag tgc ttc	96
	Pro Trp Pro Thr Leu Val Thr Thr Phe Gly Tyr Gly Leu Lys Cys Phe	
	20 25 30	
45	gcc cgc tac ccc gac cac atg aag cgg cac gac ttc ttc aag tcc gcc	144
	Ala Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser Ala	
	35 40 45	
50	atg ccc gaa ggc tac gtc cag gag cgc acc atc ttc ttc aag gac gac	192
	Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp	
	50 55 60	
55	ggc aac tac aag acc cgc gcc gag gtg aag ttc gag ggc gac acc ctg	240
	Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu	
	65 70 75 80	

	gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag gac ggc aac	288
	Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn	
	85 90 95	
5	atc ctg ggg cac aag ctg gag tac aac tac aac agc cac aac gtc tat	336
	Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr	
	100 105 110	
10	atc atg gcc gac aag cag aag aac ggc atc aag gtg aac ttc aag atc	384
	Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile	
	115 120 125	
15	cgc cac aac atc gag gac ggc agc gtg cag ctc gcc gac cac tac cag	432
	Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln	
	130 135 140	
20	cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc gac aac cac	480
	Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His	
	145 150 155 160	
25	tac ctg agc tac cag tcc gcc ctg agc aaa gac ccc aac gag aag cgc	528
	Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg	
	165 170 175	
30	gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg atc act ctc	576
	Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr Leu	
	180 185 190	
35	ggc atg gac gag ctg tac aag	597
	Gly Met Asp Glu Leu Tyr Lys	
	195	
35	YFPF2A Q69K mutation + Met @ posit. 1	
	SEQ ID NOS:50 & 51	
40	atg ggc aag ctg acc ctg aag ttc atc tgc acc acc ggc aag ctg ccc	48
	Met Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro	
	1 5 10 15	
45	gtg ccc tgg ccc acc ctc gtg acc acc ttc ggc tac ggc ctg aag tgc	96
	Val Pro Trp Pro Thr Leu Val Thr Thr Phe Gly Tyr Gly Leu Lys Cys	
	20 25 30	
50	ttc gcc cgc tac ccc gac cac atg aag cgg cac gac ttc ttc aag tcc	144
	Phe Ala Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser	
	35 40 45	
55	gcc atg ccc gaa ggc tac gtc cag gag cgc acc atc ttc ttc aag gac	192
	Ala Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp	
	50 55 60	
60	gac ggc aac tac aag acc cgc gcc gag gtg aag ttc gag ggc gac acc	240
	Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr	
	65 70 75 80	

	ctg gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag gac ggc	288
	Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly	
	85 90 95	
5	aac atc ctg ggg cac aag ctg gag tac aac tac aac agc cac aac gtc	336
	Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val	
	100 105 110	
10	tat atc atg gcc gac aag cag aag aac ggc atc aag gtg aac ttc aag	384
	Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys	
	115 120 125	
15	atc cgc cac aac atc gag gac ggc agc gtg cag ctc gcc gac cac tac	432
	Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr	
	130 135 140	
20	cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc gac aac	480
	Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn	
	145 150 155 160	
	cac tac ctg agc tac cag tcc gcc ctg agc aaa gac ccc aac gag aag	528
	His Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys	
	165 170 175	
25	cgc gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg atc act	576
	Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr	
	180 185 190	
30	ctc ggc atg gac gag ctg tac aag	600
	Leu Gly Met Asp Glu Leu Tyr Lys	
	195 200	
35	citrineF2A , V68L/ Q69K mutations	
	SEQ ID NOS:52 & 53	
40	ggc aag ctg acc ctg aag ttc atc tgc acc acc ggc aag ctg ccc gtg	48
	Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val	
	1 5 10 15	
	ccc tgg ccc acc ctc gtg acc acc ttc ggc tac ggc ctg atg tgc ttc	96
	Pro Trp Pro Thr Leu Val Thr Thr Phe Gly Tyr Gly Leu Met Cys Phe	
	20 25 30	
45	gcc cgc tac ccc gac cac atg aag cgg cac gac ttc ttc aag tcc gcc	144
	Ala Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser Ala	
	35 40 45	
50	atg ccc gaa ggc tac gtc cag gag cgc acc atc ttc ttc aag gac gac	192
	Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp	
	50 55 60	
55	ggc aac tac aag acc cgc gcc gag gtg aag ttc gag ggc gac acc ctg	240
	Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu	
	65 70 75 80	

	gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag gac ggc aac	288
	Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn	
	85 90 95	
5	atc ctg ggg cac aag ctg gag tac aac tac aac agc cac aac gtc tat	336
	Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr	
	100 105 110	
10	atc atg gcc gac aag cag aag aac ggc atc aag gtg aac ttc aag atc	384
	Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile	
	115 120 125	
15	cgc cac aac atc gag gac ggc agc gtg cag ctc gcc gac cac tac cag	432
	Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln	
	130 135 140	
20	cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc gac aac cac	480
	Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His	
	145 150 155 160	
	tac ctg agc tac cag tcc gcc ctg agc aaa gac ccc aac gag aag cgc	528
	Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg	
	165 170 175	
25	gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg atc act ctc	576
	Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr Leu	
	180 185 190	
30	ggc atg gac gag ctg tac aag	597
	Gly Met Asp Glu Leu Tyr Lys	
	195	
35	citrineF2A , V68L/ Q69K mutations + Met @ posit. 1	
	SEQ ID NOS:54 & 55	
40	atg ggc aag ctg acc ctg aag ttc atc tgc acc acc ggc aag ctg ccc	48
	Met Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro	
	1 5 10 15	
	gtg ccc tgg ccc acc ctc gtg acc acc ttc ggc tac ggc ctg atg tgc	96
	Val Pro Trp Pro Thr Leu Val Thr Thr Phe Gly Tyr Gly Leu Met Cys	
	20 25 30	
45	ttc gcc cgc tac ccc gac cac atg aag cgg cac gac ttc ttc aag tcc	144
	Phe Ala Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser	
	35 40 45	
50	gcc atg ccc gaa ggc tac gtc cag gag cgc acc atc ttc ttc aag gac	192
	Ala Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp	
	50 55 60	
55	gac ggc aac tac aag acc cgc gcc gag gtg aag ttc gag ggc gac acc	240
	Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr	
	65 70 75 80	

	ctg gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag gac ggc	288
	Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly	
	85 90 95	
5	aac atc ctg ggg cac aag ctg gag tac aac tac aac agc cac aac gtc	336
	Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val	
	100 105 110	
10	tat atc atg gcc gac aag cag aag aac ggc atc aag gtg aac ttc aag	384
	Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys	
	115 120 125	
15	atc cgc cac aac atc gag gac ggc agc gtg cag ctc gcc gac cac tac	432
	Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr	
	130 135 140	
20	cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc gac aac	480
	Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn	
	145 150 155 160	
	cac tac ctg agc tac cag tcc gcc ctg agc aaa gac ccc aac gag aag	528
	His Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys	
	165 170 175	
25	cgc gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg atc act	576
	Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr	
	180 185 190	
30	ctc ggc atg gac gag ctg tac aag	600
	Leu Gly Met Asp Glu Leu Tyr Lys	
	195 200	
35	citrine/VenusF2A , V68L/Q69K/N146I/M153T/V163A mutations	
	SEQ ID NOS:56 & 57	
40	ggc aag ctg acc ctg aag ttc atc tgc acc acc ggc aag ctg ccc gtg	48
	Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val	
	1 5 10 15	
	ccc tgg ccc acc ctc gtg acc acc ttc ggc tac ggc ctg atg tgc ttc	96
	Pro Trp Pro Thr Leu Val Thr Thr Phe Gly Tyr Gly Leu Met Cys Phe	
	20 25 30	
45	gcc cgc tac ccc gac cac atg aag cgg cac gac ttc ttc aag tcc gcc	144
	Ala Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser Ala	
	35 40 45	
50	atg ccc gaa ggc tac gtc cag gag cgc acc atc ttc ttc aag gac gac	192
	Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp	
	50 55 60	
55	ggc aac tac aag acc cgc gcc gag gtg aag ttc gag ggc gac acc ctg	240
	Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu	
	65 70 75 80	



	gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag gac ggc aac	288
	Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn	
	85 90 95	
5	atc ctg ggg cac aag ctg gag tac aac tac atc agc cac aac gtc tat	336
	Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Ile Ser His Asn Val Tyr	
	100 105 110	
10	atc acc gcc gac aag cag aag aac ggc atc aag gcc aac ttc aag atc	384
	Ile Thr Ala Asp Lys Gln Lys Asn Gly Ile Lys Ala Asn Phe Lys Ile	
	115 120 125	
15	cgc cac aac atc gag gac ggc agc gtg cag ctc gcc gac cac tac cag	432
	Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln	
	130 135 140	
20	cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc gac aac cac	480
	Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His	
	145 150 155 160	
	tac ctg agc tac cag tcc gcc ctg agc aaa gac ccc aac gag aag cgc	528
	Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg	
	165 170 175	
25	gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg atc act ctc	576
	Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr Leu	
	180 185 190	
30	ggc atg gac gag ctg tac aag	597
	Gly Met Asp Glu Leu Tyr Lys	
	195	
35	citrine/Venus F2A V68L/Q69K/N146I/M153T/V163A + Met @ pos. 1	
	SEQ ID NOS:58 & 59	
40	atg ggc aag ctg acc ctg aag ttc atc tgc acc acc ggc aag ctg ccc	48
	Met Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro	
	1 5 10 15	
	gtg ccc tgg ccc acc ctc gtg acc acc ttc ggc tac ggc ctg atg tgc	96
	Val Pro Trp Pro Thr Leu Val Thr Thr Phe Gly Tyr Gly Leu Met Cys	
	20 25 30	
45	ttc gcc cgc tac ccc gac cac atg aag cgg cac gac ttc ttc aag tcc	144
	Phe Ala Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser	
	35 40 45	
50	gcc atg ccc gaa ggc tac gtc cag gag cgc acc atc ttc ttc aag gac	192
	Ala Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp	
	50 55 60	
55	gac ggc aac tac aag acc cgc gcc gag gtg aag ttc gag ggc gac acc	240
	Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr	
	65 70 75 80	

	ctg gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag gac ggc	288
	Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly	
	85 90 95	
5	aac atc ctg ggg cac aag ctg gag tac aac tac atc agc cac aac gtc	336
	Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Ile Ser His Asn Val	
	100 105 110	
10	tat atc acc gcc gac aag cag aag aac ggc atc aag gcc aac ttc aag	384
	Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly Ile Lys Ala Asn Phe Lys	
	115 120 125	
15	atc cgc cac aac atc gag gac ggc agc gtg cag ctc gcc gac cac tac	432
	Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr	
	130 135 140	
20	cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc gac aac	480
	Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn	
	145 150 155 160	
	cac tac ctg agc tac cag tcc gcc ctg agc aaa gac ccc aac gag aag	528
	His Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys	
	165 170 175	
25	cgc gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg atc act	576
	Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr	
	180 185 190	
30	ctc ggc atg gac gag ctg tac aag	600
	Leu Gly Met Asp Glu Leu Tyr Lys	
	195 200	
35	CFP F2A, F64L mutation	
	SEQ ID NOS:60 & 61	
40	ggc aag ctg acc ctg aag ttc atc tgc acc acc ggc aag ctg ccc gtg	48
	Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val	
	1 5 10 15	
	ccc tgg ccc acc ctc gtg acc acc ctg ggc tac ggc ctg cag tgc ttc	96
	Pro Trp Pro Thr Leu Val Thr Thr Leu Gly Tyr Gly Leu Gln Cys Phe	
	20 25 30	
45	gcc cgc tac ccc gac cac atg aag cgg cac gac ttc ttc aag tcc gcc	144
	Ala Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser Ala	
	35 40 45	
50	atg ccc gaa ggc tac gtc cag gag cgc acc atc ttc ttc aag gac gac	192
	Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp	
	50 55 60	
55	ggc aac tac aag acc cgc gcc gag gtg aag ttc gag ggc gac acc ctg	240
	Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu	
	65 70 75 80	

	gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag gac ggc aac	288
	Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn	
	85 90 95	
5	atc ctg ggg cac aag ctg gag tac aac tac aac agc cac aac gtc tat	336
	Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr	
	100 105 110	
10	atc atg gcc gac aag cag aag aac ggc atc aag gtg aac ttc aag atc	384
	Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile	
	115 120 125	
15	cgc cac aac atc gag gac ggc agc gtg cag ctc gcc gac cac tac cag	432
	Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln	
	130 135 140	
20	cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc gac aac cac	480
	Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His	
	145 150 155 160	
	tac ctg agc tac cag tcc gcc ctg agc aaa gac ccc aac gag aag cgc	528
	Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg	
	165 170 175	
25	gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg atc act ctc	576
	Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr Leu	
	180 185 190	
30	ggc atg gac gag ctg tac aag	597
	Gly Met Asp Glu Leu Tyr Lys	
	195	
35	CFP F2A, F64L mutation + Met @ posit. 1	
	SEQ ID NOS:62 & 63	
40	atg ggc aag ctg acc ctg aag ttc atc tgc acc acc ggc aag ctg ccc	48
	Met Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro	
	1 5 10 15	
	gtg ccc tgg ccc acc ctc gtg acc acc ctg ggc tac ggc ctg cag tgc	96
	Val Pro Trp Pro Thr Leu Val Thr Thr Leu Gly Tyr Gly Leu Gln Cys	
	20 25 30	
45	ttc gcc cgc tac ccc gac cac atg aag cgg cac gac ttc ttc aag tcc	144
	Phe Ala Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser	
	35 40 45	
50	gcc atg ccc gaa ggc tac gtc cag gag cgc acc atc ttc ttc aag gac	192
	Ala Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp	
	50 55 60	
55	gac ggc aac tac aag acc cgc gcc gag gtg aag ttc gag ggc gac acc	240
	Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr	
	65 70 75 80	

	ctg gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag gac ggc	288
	Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly	
	85 90 95	
5	aac atc ctg ggg cac aag ctg gag tac aac tac aac agc cac aac gtc	336
	Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val	
	100 105 110	
10	tat atc atg gcc gac aag cag aag aac ggc atc aag gtg aac ttc aag	384
	Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys	
	115 120 125	
15	atc cgc cac aac atc gag gac ggc agc gtg cag ctc gcc gac cac tac	432
	Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr	
	130 135 140	
20	cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc gac aac	480
	Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn	
	145 150 155 160	
	cac tac ctg agc tac cag tcc gcc ctg agc aaa gac ccc aac gag aag	528
	His Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys	
	165 170 175	
25	cgc gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg atc act	576
	Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr	
	180 185 190	
30	ctc ggc atg gac gag ctg tac aag	600
	Leu Gly Met Asp Glu Leu Tyr Lys	
	195 200	
35	CFP F2A , Y66W mutation	
	SEQ ID NOS:64 & 65	
40	ggc aag ctg acc ctg aag ttc atc tgc acc acc ggc aag ctg ccc gtg	48
	Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val	
	1 5 10 15	
	ccc tgg ccc acc ctc gtg acc acc ttc ggc tgg ggc ctg cag tgc ttc	96
	Pro Trp Pro Thr Leu Val Thr Thr Phe Gly Trp Gly Leu Gln Cys Phe	
	20 25 30	
45	gcc cgc tac ccc gac cac atg aag cgg cac gac ttc ttc aag tcc gcc	144
	Ala Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser Ala	
	35 40 45	
50	atg ccc gaa ggc tac gtc cag gag cgc acc atc ttc ttc aag gac gac	192
	Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp	
	50 55 60	
55	ggc aac tac aag acc cgc gcc gag gtg aag ttc gag ggc gac acc ctg	240
	Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu	
	65 70 75 80	

	gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag gac ggc aac	288
	Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn	
	85 90 95	
5	atc ctg ggg cac aag ctg gag tac aac tac aac agc cac aac gtc tat	336
	Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr	
	100 105 110	
10	atc atg gcc gac aag cag aag aac ggc atc aag gtg aac ttc aag atc	384
	Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile	
	115 120 125	
15	cgc cac aac atc gag gac ggc agc gtg cag ctc gcc gac cac tac cag	432
	Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln	
	130 135 140	
20	cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc gac aac cac	480
	Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His	
	145 150 155 160	
	tac ctg agc tac cag tcc gcc ctg agc aaa gac ccc aac gag aag cgc	528
	Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg	
	165 170 175	
25	gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg atc act ctc	576
	Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr Leu	
	180 185 190	
30	ggc atg gac gag ctg tac aag	597
	Gly Met Asp Glu Leu Tyr Lys	
	195	
35	CFP F2A , Y66W mutation + Met @ posit. 1	
	SEQ ID NOS:66 & 67	
40	atg ggc aag ctg acc ctg aag ttc atc tgc acc acc ggc aag ctg ccc	48
	Met Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro	
	1 5 10 15	
	gtg ccc tgg ccc acc ctc gtg acc acc ttc ggc tgg ggc ctg cag tgc	96
	Val Pro Trp Pro Thr Leu Val Thr Thr Phe Gly Trp Gly Leu Gln Cys	
	20 25 30	
45	ttc gcc cgc tac ccc gac cac atg aag cgg cac gac ttc ttc aag tcc	144
	Phe Ala Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser	
	35 40 45	
50	gcc atg ccc gaa ggc tac gtc cag gag cgc acc atc ttc ttc aag gac	192
	Ala Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp	
	50 55 60	
55	gac ggc aac tac aag acc cgc gcc gag gtg aag ttc gag ggc gac acc	240
	Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr	
	65 70 75 80	

	ctg gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag gac ggc	288
	Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly	
	85 90 95	
5	aac atc ctg ggg cac aag ctg gag tac aac tac aac agc cac aac gtc	336
	Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val	
	100 105 110	
10	tat atc atg gcc gac aag cag aag aac ggc atc aag gtg aac ttc aag	384
	Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys	
	115 120 125	
15	atc cgc cac aac atc gag gac ggc agc gtg cag ctc gcc gac cac tac	432
	Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr	
	130 135 140	
20	cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc gac aac	480
	Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn	
	145 150 155 160	
	cac tac ctg agc tac cag tcc gcc ctg agc aaa gac ccc aac gag aag	528
	His Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys	
	165 170 175	
25	cgc gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg atc act	576
	Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr	
	180 185 190	
30	ctc ggc atg gac gag ctg tac aag	600
	Leu Gly Met Asp Glu Leu Tyr Lys	
	195 200	
35	CFP F2A , S65A mutation	
	SEQ ID NOS:68 & 69	
40	ggc aag ctg acc ctg aag ttc atc tgc acc acc ggc aag ctg ccc gtg	48
	Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val	
	1 5 10 15	
	ccc tgg ccc acc ctc gtg acc acc ttc gcc tac ggc ctg cag tgc ttc	96
	Pro Trp Pro Thr Leu Val Thr Thr Phe Ala Tyr Gly Leu Gln Cys Phe	
	20 25 30	
45	gcc cgc tac ccc gac cac atg aag cgg cac gac ttc ttc aag tcc gcc	144
	Ala Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser Ala	
	35 40 45	
50	atg ccc gaa ggc tac gtc cag gag cgc acc atc ttc ttc aag gac gac	192
	Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp	
	50 55 60	
55	ggc aac tac aag acc cgc gcc gag gtg aag ttc gag ggc gac acc ctg	240
	Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu	
	65 70 75 80	

	gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag gac ggc aac	288
	Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn	
	85 90 95	
5	atc ctg ggg cac aag ctg gag tac aac tac aac agc cac aac gtc tat	336
	Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr	
	100 105 110	
10	atc atg gcc gac aag cag aag aac ggc atc aag gtg aac ttc aag atc	384
	Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile	
	115 120 125	
15	cgc cac aac atc gag gac ggc agc gtg cag ctc gcc gac cac tac cag	432
	Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln	
	130 135 140	
20	cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc gac aac cac	480
	Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His	
	145 150 155 160	
	tac ctg agc tac cag tcc gcc ctg agc aaa gac ccc aac gag aag cgc	528
	Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg	
	165 170 175	
25	gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg atc act ctc	576
	Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr Leu	
	180 185 190	
30	ggc atg gac gag ctg tac aag	597
	Gly Met Asp Glu Leu Tyr Lys	
	195	
35	CFP F2A , S65A mutation + Met @ posit 1	
	SEQ ID NOS:70 & 71	
40	atg ggc aag ctg acc ctg aag ttc atc tgc acc acc ggc aag ctg ccc	48
	Met Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro	
	1 5 10 15	
	gtg ccc tgg ccc acc ctc gtg acc acc ttc gcc tac ggc ctg cag tgc	96
	Val Pro Trp Pro Thr Leu Val Thr Thr Phe Ala Tyr Gly Leu Gln Cys	
	20 25 30	
45	ttc gcc cgc tac ccc gac cac atg aag cgg cac gac ttc ttc aag tcc	144
	Phe Ala Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser	
	35 40 45	
50	gcc atg ccc gaa ggc tac gtc cag gag cgc acc atc ttc ttc aag gac	192
	Ala Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp	
	50 55 60	
55	gac ggc aac tac aag acc cgc gcc gag gtg aag ttc gag ggc gac acc	240
	Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr	
	65 70 75 80	

	ctg gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag gac ggc	288
	Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly	
	85 90 95	
5	aac atc ctg ggg cac aag ctg gag tac aac tac aac agc cac aac gtc	336
	Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val	
	100 105 110	
10	tat atc atg gcc gac aag cag aag aac ggc atc aag gtg aac ttc aag	384
	Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys	
	115 120 125	
15	atc cgc cac aac atc gag gac ggc agc gtg cag ctc gcc gac cac tac	432
	Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr	
	130 135 140	
20	cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc gac aac	480
	Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn	
	145 150 155 160	
	cac tac ctg agc tac cag tcc gcc ctg agc aaa gac ccc aac gag aag	528
	His Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys	
	165 170 175	
25	cgc gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg atc act	576
	Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr	
	180 185 190	
30	ctc ggc atg gac gag ctg tac aag	600
	Leu Gly Met Asp Glu Leu Tyr Lys	
	195 200	
35	CGFP F2A ,S65A/Y66W/T203Y mutations	
	SEQ ID NOS:72 & 73	
40	ggc aag ctg acc ctg aag ttc atc tgc acc acc ggc aag ctg ccc gtg	48
	Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val	
	1 5 10 15	
	ccc tgg ccc acc ctc gtg acc acc ttc gcc tgg ggc ctg cag tgc ttc	96
	Pro Trp Pro Thr Leu Val Thr Thr Phe Ala Trp Gly Leu Gln Cys Phe	
	20 25 30	
45	gcc cgc tac ccc gac cac atg aag cgg cac gac ttc ttc aag tcc gcc	144
	Ala Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser Ala	
	35 40 45	
50	atg ccc gaa ggc tac gtc cag gag cgc acc atc ttc ttc aag gac gac	192
	Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp	
	50 55 60	
55	ggc aac tac aag acc cgc gcc gag gtg aag ttc gag ggc gac acc ctg	240
	Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu	
	65 70 75 80	



	gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag gac ggc aac	288
	Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn	
	85 90 95	
5	atc ctg ggg cac aag ctg gag tac aac tac aac agc cac aac gtc tat	336
	Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr	
	100 105 110	
10	atc atg gcc gac aag cag aag aac ggc atc aag gtg aac ttc aag atc	384
	Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile	
	115 120 125	
15	cgc cac aac atc gag gac ggc agc gtg cag ctc gcc gac cac tac cag	432
	Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln	
	130 135 140	
20	cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc gac aac cac	480
	Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His	
	145 150 155 160	
	tac ctg agc tac cag tcc gcc ctg agc aaa gac ccc aac gag aag cgc	528
	Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg	
	165 170 175	
25	gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg atc act ctc	576
	Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr Leu	
	180 185 190	
30	ggc atg gac gag ctg tac aag	597
	Gly Met Asp Glu Leu Tyr Lys	
	195	
35	CGFP F2A ,S65A/Y66W/T203Y mutations + Met @ pos. 1	
	SEQ ID NOS:74 & 75	
40	atg ggc aag ctg acc ctg aag ttc atc tgc acc acc ggc aag ctg ccc	48
	Met Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro	
	1 5 10 15	
	gtg ccc tgg ccc acc ctc gtg acc acc ttc gcc tgg ggc ctg cag tgc	96
	Val Pro Trp Pro Thr Leu Val Thr Thr Phe Ala Trp Gly Leu Gln Cys	
	20 25 30	
45	ttc gcc cgc tac ccc gac cac atg aag cgg cac gac ttc ttc aag tcc	144
	Phe Ala Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser	
	35 40 45	
50	gcc atg ccc gaa ggc tac gtc cag gag cgc acc atc ttc ttc aag gac	192
	Ala Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp	
	50 55 60	
55	gac ggc aac tac aag acc cgc gcc gag gtg aag ttc gag ggc gac acc	240
	Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr	
	65 70 75 80	

	ctg gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag gac ggc	288
	Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly	
	85 90 95	
5	aac atc ctg ggg cac aag ctg gag tac aac tac aac agc cac aac gtc	336
	Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val	
	100 105 110	
10	tat atc atg gcc gac aag cag aag aac ggc atc aag gtg aac ttc aag	384
	Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys	
	115 120 125	
15	atc cgc cac aac atc gag gac ggc agc gtg cag ctc gcc gac cac tac	432
	Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr	
	130 135 140	
20	cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc gac aac	480
	Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn	
	145 150 155 160	
	cac tac ctg agc tac cag tcc gcc ctg agc aaa gac ccc aac gag aag	528
	His Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys	
	165 170 175	
25	cgc gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg atc act	576
	Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr	
	180 185 190	
30	ctc ggc atg gac gag ctg tac aag	600
	Leu Gly Met Asp Glu Leu Tyr Lys	
	195 200	
35	CGFP F2A ,F64L/S65T/Y66W/M153T/V163A/T203Y mutations	
	SEQ ID NOS:76 & 77	
40	ggc aag ctg acc ctg aag ttc atc tgc acc acc ggc aag ctg ccc gtg	48
	Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val	
	1 5 10 15	
45	ccc tgg ccc acc ctc gtg acc acc ctg acc tgg ggc ctg cag tgc ttc	96
	Pro Trp Pro Thr Leu Val Thr Thr Leu Thr Trp Gly Leu Gln Cys Phe	
	20 25 30	
	gcc cgc tac ccc gac cac atg aag cgg cac gac ttc ttc aag tcc gcc	144
	Ala Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser Ala	
	35 40 45	
50	atg ccc gaa ggc tac gtc cag gag cgc acc atc ttc ttc aag gac gac	192
	Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp	
	50 55 60	
55	ggc aac tac aag acc cgc gcc gag gtg aag ttc gag ggc gac acc ctg	240
	Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu	
	65 70 75 80	

	gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag gac ggc aac	288
	Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn	
	85 90 95	
5	atc ctg ggg cac aag ctg gag tac aac tac aac agc cac aac gtc tat	336
	Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr	
	100 105 110	
10	atc acc gcc gac aag cag aag aac ggc atc aag gcc aac ttc aag atc	384
	Ile Thr Ala Asp Lys Gln Lys Asn Gly Ile Lys Ala Asn Phe Lys Ile	
	115 120 125	
15	cgc cac aac atc gag gac ggc agc gtg cag ctc gcc gac cac tac cag	432
	Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln	
	130 135 140	
20	cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc gac aac cac	480
	Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His	
	145 150 155 160	
25	tac ctg agc tac cag tcc gcc ctg agc aaa gac ccc aac gag aag cgc	528
	Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg	
	165 170 175	
30	gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg atc act ctc	576
	Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr Leu	
	180 185 190	
35	ggc atg gac gag ctg tac aag	597
	Gly Met Asp Glu Leu Tyr Lys	
	195	
35	CGFP F2A,F64L/S65T/Y66W/M153T/V163A/T203Y mutations + Met @ pos. 1	
40	78	
	atg ggc aag ctg acc ctg aag ttc atc tgc acc acc ggc aag ctg ccc	48
	Met Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro	
	1 5 10 15	
45	gtg ccc tgg ccc acc ctc gtg acc acc ctg acc tgg ggc ctg cag tgc	96
	Val Pro Trp Pro Thr Leu Val Thr Thr Leu Thr Trp Gly Leu Gln Cys	
	20 25 30	
50	ttc gcc cgc tac ccc gac cac atg aag cgg cac gac ttc ttc aag tcc	144
	Phe Ala Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser	
	35 40 45	
55	gcc atg ccc gaa ggc tac gtc cag gag cgc acc atc ttc ttc aag gac	192
	Ala Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp	
	50 55 60	
55	gac ggc aac tac aag acc cgc gcc gag gtg aag ttc gag ggc gac acc	240
	Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr	
	65 70 75 80	

	ctg gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag gac ggc	288
	Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly	
	85 90 95	
5	aac atc ctg ggg cac aag ctg gag tac aac tac aac agc cac aac gtc	336
	Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val	
	100 105 110	
10	tat atc acc gcc gac aag cag aag aac ggc atc aag gcc aac ttc aag	384
	Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly Ile Lys Ala Asn Phe Lys	
	115 120 125	
15	atc cgc cac aac atc gag gac ggc agc gtg cag ctc gcc gac cac tac	432
	Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr	
	130 135 140	
20	cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc gac aac	480
	Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn	
	145 150 155 160	
	cac tac ctg agc tac cag tcc gcc ctg agc aaa gac ccc aac gag aag	528
	His Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys	
	165 170 175	
25	cgc gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg atc act	576
	Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr	
	180 185 190	
30	ctc ggc atg gac gag ctg tac aag	600
	Leu Gly Met Asp Glu Leu Tyr Lys	
	195 200	
35	CFP F2A,F46L/S65T/Y66W/N146I/M153T/V163A mutations	
	SEQ ID NOS:80 & 81	
40	ggc aag ctg acc ctg aag ttc atc tgc acc acc ggc aag ctg ccc gtg	48
	Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val	
	1 5 10 15	
	ccc tgg ccc acc ctc gtg acc acc ctg acc tgg ggc ctg cag tgc ttc	96
	Pro Trp Pro Thr Leu Val Thr Thr Leu Thr Trp Gly Leu Gln Cys Phe	
	20 25 30	
45	gcc cgc tac ccc gac cac atg aag cgg cac gac ttc ttc aag tcc gcc	144
	Ala Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser Ala	
	35 40 45	
50	atg ccc gaa ggc tac gtc cag gag cgc acc atc ttc ttc aag gac gac	192
	Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp	
	50 55 60	
55	ggc aac tac aag acc cgc gcc gag gtg aag ttc gag ggc gac acc ctg	240
	Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu	
	65 70 75 80	

	gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag gac ggc aac	288
	Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn	
	85 90 95	
5	atc ctg ggg cac aag ctg gag tac aac tac atc agc cac aac gtc tat	336
	Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Ile Ser His Asn Val Tyr	
	100 105 110	
10	atc acc gcc gac aag cag aag aac ggc atc aag gcc aac ttc aag atc	384
	Ile Thr Ala Asp Lys Gln Lys Asn Gly Ile Lys Ala Asn Phe Lys Ile	
	115 120 125	
15	cgc cac aac atc gag gac ggc agc gtg cag ctc gcc gac cac tac cag	432
	Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln	
	130 135 140	
20	cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc gac aac cac	480
	Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His	
	145 150 155 160	
	tac ctg agc acc cag tcc gcc ctg agc aaa gac ccc aac gag aag cgc	528
	Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg	
	165 170 175	
25	gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg atc act ctc	576
	Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr Leu	
	180 185 190	
30	ggc atg gac gag ctg tac aag	597
	Gly Met Asp Glu Leu Tyr Lys	
	195	
35	CFP F2A, F2A,F46L/S65T/Y66W/N146I/M153T/V163A mutations + Met @ pos. 1	
	SEQ ID NOS:82 & 83	
40	atg ggc aag ctg acc ctg aag ttc atc tgc acc acc ggc aag ctg ccc	48
	Met Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro	
	1 5 10 15	
	gtg ccc tgg ccc acc ctc gtg acc acc ctg acc tgg ggc ctg cag tgc	96
	Val Pro Trp Pro Thr Leu Val Thr Thr Leu Thr Trp Gly Leu Gln Cys	
	20 25 30	
45	ttc gcc cgc tac ccc gac cac atg aag cgg cac gac ttc ttc aag tcc	144
	Phe Ala Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser	
	35 40 45	
50	gcc atg ccc gaa ggc tac gtc cag gag cgc acc atc ttc ttc aag gac	192
	Ala Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp	
	50 55 60	
55	gac ggc aac tac aag acc cgc gcc gag gtg aag ttc gag ggc gac acc	240
	Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr	
	65 70 75 80	

	ctg gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag gac ggc	288
	Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly	
	85 90 95	
5	aac atc ctg ggg cac aag ctg gag tac aac tac atc agc cac aac gtc	336
	Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Ile Ser His Asn Val	
	100 105 110	
10	tat atc acc gcc gac aag cag aag aac ggc atc aag gcc aac ttc aag	384
	Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly Ile Lys Ala Asn Phe Lys	
	115 120 125	
15	atc cgc cac aac atc gag gac ggc agc gtg cag ctc gcc gac cac tac	432
	Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr	
	130 135 140	
20	cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc gac aac	480
	Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn	
	145 150 155 160	
	cac tac ctg agc acc cag tcc gcc ctg agc aaa gac ccc aac gag aag	528
	His Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys	
	165 170 175	
25	cgc gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg atc act	576
	Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr	
	180 185 190	
30	ctc ggc atg gac gag ctg tac aag	600
	Leu Gly Met Asp Glu Leu Tyr Lys	
	195 200	
35	CFP F2A, N146I mutation	
	SEQ ID NOS:84 & 85	
40	ggc aag ctg acc ctg aag ttc atc tgc acc acc ggc aag ctg ccc gtg	48
	Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val	
	1 5 10 15	
	ccc tgg ccc acc ctc gtg acc acc ttc ggc tac ggc ctg cag tgc ttc	96
	Pro Trp Pro Thr Leu Val Thr Thr Phe Gly Tyr Gly Leu Gln Cys Phe	
	20 25 30	
45	gcc cgc tac ccc gac cac atg aag cgg cac gac ttc ttc aag tcc gcc	144
	Ala Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser Ala	
	35 40 45	
50	atg ccc gaa ggc tac gtc cag gag cgc acc atc ttc ttc aag gac gac	192
	Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp	
	50 55 60	
55	ggc aac tac aag acc cgc gcc gag gtg aag ttc gag ggc gac acc ctg	240
	Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu	
	65 70 75 80	

	gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag gac ggc aac	288
	Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn	
	85 90 95	
5	atc ctg ggg cac aag ctg gag tac aac tac atc agc cac aac gtc tat	336
	Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Ile Ser His Asn Val Tyr	
	100 105 110	
10	atc atg gcc gac aag cag aag aac ggc atc aag gtg aac ttc aag atc	384
	Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile	
	115 120 125	
15	cgc cac aac atc gag gac ggc agc gtg cag ctc gcc gac cac tac cag	432
	Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln	
	130 135 140	
20	cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc gac aac cac	480
	Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His	
	145 150 155 160	
25	tac ctg agc acc cag tcc gcc ctg agc aaa gac ccc aac gag aag cgc	528
	Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg	
	165 170 175	
30	gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg atc act ctc	576
	Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr Leu	
	180 185 190	
35	ggc atg gac gag ctg tac aag	597
	Gly Met Asp Glu Leu Tyr Lys	
	195	
40	CFP F2A, N146I mutation + Met @ posit. 1	
	SEQ ID NOS:86 & 87	
45	atg ggc aag ctg acc ctg aag ttc atc tgc acc acc ggc aag ctg ccc	48
	Met Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro	
	1 5 10 15	
50	gtg ccc tgg ccc acc ctc gtg acc acc ttc ggc tac ggc ctg cag tgc	96
	Val Pro Trp Pro Thr Leu Val Thr Thr Phe Gly Tyr Gly Leu Gln Cys	
	20 25 30	
55	ttc gcc cgc tac ccc gac cac atg aag cgg cac gac ttc ttc aag tcc	144
	Phe Ala Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser	
	35 40 45	
60	gcc atg ccc gaa ggc tac gtc cag gag cgc acc atc ttc ttc aag gac	192
	Ala Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp	
	50 55 60	
65	gac ggc aac tac aag acc cgc gcc gag gtg aag ttc gag ggc gac acc	240
	Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr	
	65 70 75 80	

	ctg gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag gac ggc	288
	Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly	
	85 90 95	
5	aac atc ctg ggg cac aag ctg gag tac aac tac atc agc cac aac gtc	336
	Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Ile Ser His Asn Val	
	100 105 110	
10	tat atc atg gcc gac aag cag aag aac ggc atc aag gtg aac ttc aag	384
	Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys	
	115 120 125	
15	atc cgc cac aac atc gag gac ggc agc gtg cag ctc gcc gac cac tac	432
	Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr	
	130 135 140	
20	cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc gac aac	480
	Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn	
	145 150 155 160	
	cac tac ctg agc acc cag tcc gcc ctg agc aaa gac ccc aac gag aag	528
	His Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys	
	165 170 175	
25	cgc gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg atc act	576
	Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr	
	180 185 190	
30	ctc ggc atg gac gag ctg tac aag	600
	Leu Gly Met Asp Glu Leu Tyr Lys	
	195 200	
35	CFP F2A, M153T mutation SEQ ID NOS:88 & 89	
40	ggc aag ctg acc ctg aag ttc atc tgc acc acc ggc aag ctg ccc gtg	48
	Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val	
	1 5 10 15	
	ccc tgg ccc acc ctc gtg acc acc ttc ggc tac ggc ctg cag tgc ttc	96
	Pro Trp Pro Thr Leu Val Thr Thr Phe Gly Tyr Gly Leu Gln Cys Phe	
	20 25 30	
45	gcc cgc tac ccc gac cac atg aag cgg cac gac ttc ttc aag tcc gcc	144
	Ala Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser Ala	
	35 40 45	
50	atg ccc gaa ggc tac gtc cag gag cgc acc atc ttc ttc aag gac gac	192
	Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp	
	50 55 60	
55	ggc aac tac aag acc cgc gcc gag gtg aag ttc gag ggc gac acc ctg	240
	Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu	
	65 70 75 80	



	gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag gac ggc aac	288
	Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn	
	85 90 95	
5	atc ctg ggg cac aag ctg gag tac aac tac aac agc cac aac gtc tat	336
	Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr	
	100 105 110	
10	atc acc gcc gac aag cag aag aac ggc atc aag gtg aac ttc aag atc	384
	Ile Thr Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile	
	115 120 125	
15	cgc cac aac atc gag gac ggc agc gtg cag ctc gcc gac cac tac cag	432
	Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln	
	130 135 140	
20	cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc gac aac cac	480
	Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His	
	145 150 155 160	
	tac ctg agc acc cag tcc gcc ctg agc aaa gac ccc aac gag aag cgc	528
	Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg	
	165 170 175	
25	gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg atc act ctc	576
	Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr Leu	
	180 185 190	
30	ggc atg gac gag ctg tac aag	597
	Gly Met Asp Glu Leu Tyr Lys	
	195	
35	CFP F2A, M153T mutation + Met @ posit. 1	
	SEQ ID NOS:90 & 91	
40	atg ggc aag ctg acc ctg aag ttc atc tgc acc acc ggc aag ctg ccc	48
	Met Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro	
	1 5 10 15	
45	gtg ccc tgg ccc acc ctc gtg acc acc ttc ggc tac ggc ctg cag tgc	96
	Val Pro Trp Pro Thr Leu Val Thr Thr Phe Gly Tyr Gly Leu Gln Cys	
	20 25 30	
	ttc gcc cgc tac ccc gac cac atg aag cgg cac gac ttc ttc aag tcc	144
	Phe Ala Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser	
	35 40 45	
50	gcc atg ccc gaa ggc tac gtc cag gag cgc acc atc ttc ttc aag gac	192
	Ala Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp	
	50 55 60	
55	gac ggc aac tac aag acc cgc gcc gag gtg aag ttc gag ggc gac acc	240
	Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr	
	65 70 75 80	

	ctg gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag gac ggc	288
	Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly	
	85 90 95	
5	aac atc ctg ggg cac aag ctg gag tac aac tac aac agc cac aac gtc	336
	Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val	
	100 105 110	
10	tat atc acc gcc gac aag cag aag aac ggc atc aag gtg aac ttc aag	384
	Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys	
	115 120 125	
15	atc cgc cac aac atc gag gac ggc agc gtg cag ctc gcc gac cac tac	432
	Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr	
	130 135 140	
20	cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc gac aac	480
	Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn	
	145 150 155 160	
	cac tac ctg agc acc cag tcc gcc ctg agc aaa gac ccc aac gag aag	528
	His Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys	
	165 170 175	
25	cgc gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg atc act	576
	Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr	
	180 185 190	
30	ctc ggc atg gac gag ctg tac aag	600
	Leu Gly Met Asp Glu Leu Tyr Lys	
	195 200	
35	CFP F2A ,N146I/ M153T mutations	
	SEQ ID NOS:92 & 93	
40	ggc aag ctg acc ctg aag ttc atc tgc acc acc ggc aag ctg ccc gtg	48
	Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val	
	1 5 10 15	
	ccc tgg ccc acc ctc gtg acc acc ttc ggc tac ggc ctg cag tgc ttc	96
	Pro Trp Pro Thr Leu Val Thr Thr Phe Gly Tyr Gly Leu Gln Cys Phe	
	20 25 30	
45	gcc cgc tac ccc gac cac atg aag cgg cac gac ttc ttc aag tcc gcc	144
	Ala Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser Ala	
	35 40 45	
50	atg ccc gaa ggc tac gtc cag gag cgc acc atc ttc ttc aag gac gac	192
	Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp	
	50 55 60	
55	ggc aac tac aag acc cgc gcc gag gtg aag ttc gag ggc gac acc ctg	240
	Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu	
	65 70 75 80	

	gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag gac ggc aac	288
	Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn	
	85 90 95	
5	atc ctg ggg cac aag ctg gag tac aac tac atc agc cac aac gtc tat	336
	Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Ile Ser His Asn Val Tyr	
	100 105 110	
10	atc acc gcc gac aag cag aag aac ggc atc aag gtg aac ttc aag atc	384
	Ile Thr Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile	
	115 120 125	
15	cgc cac aac atc gag gac ggc agc gtg cag ctc gcc gac cac tac cag	432
	Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln	
	130 135 140	
20	cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc gac aac cac	480
	Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His	
	145 150 155 160	
	tac ctg agc acc cag tcc gcc ctg agc aaa gac ccc aac gag aag cgc	528
	Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg	
	165 170 175	
25	gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg atc act ctc	576
	Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr Leu	
	180 185 190	
30	ggc atg gac gag ctg tac aag	597
	Gly Met Asp Glu Leu Tyr Lys	
	195	
35	CFP F2A ,N146I/ M153T mutations +Met @ posit. 1	
	SEQ ID NOS:94 & 95	
40	atg ggc aag ctg acc ctg aag ttc atc tgc acc acc ggc aag ctg ccc	48
	Met Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro	
	1 5 10 15	
45	gtg ccc tgg ccc acc ctc gtg acc acc ttc ggc tac ggc ctg cag tgc	96
	Val Pro Trp Pro Thr Leu Val Thr Thr Phe Gly Tyr Gly Leu Gln Cys	
	20 25 30	
	ttc gcc cgc tac ccc gac cac atg aag cgg cac gac ttc ttc aag tcc	144
	Phe Ala Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser	
	35 40 45	
50	gcc atg ccc gaa ggc tac gtc cag gag cgc acc atc ttc ttc aag gac	192
	Ala Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp	
	50 55 60	
55	gac ggc aac tac aag acc cgc gcc gag gtg aag ttc gag ggc gac acc	240
	Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr	
	65 70 75 80	

	ctg gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag gac ggc	288
	Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly	
	85 90 95	
5	aac atc ctg ggg cac aag ctg gag tac aac tac atc agc cac aac gtc	336
	Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Ile Ser His Asn Val	
	100 105 110	
10	tat atc acc gcc gac aag cag aag aac ggc atc aag gtg aac ttc aag	384
	Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys	
	115 120 125	
15	atc cgc cac aac atc gag gac ggc agc gtg cag ctc gcc gac cac tac	432
	Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr	
	130 135 140	
20	cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc gac aac	480
	Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn	
	145 150 155 160	
	cac tac ctg agc acc cag tcc gcc ctg agc aaa gac ccc aac gag aag	528
	His Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys	
	165 170 175	
25	cgc gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg atc act	576
	Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr	
	180 185 190	
30	ctc ggc atg gac gag ctg tac aag	600
	Leu Gly Met Asp Glu Leu Tyr Lys	
	195 200	
35	CFP F2A ,F64L/S65T/Y66W/N146I/M153T mutations	
	SEQ ID NOS:96 & 97	
40	ggc aag ctg acc ctg aag ttc atc tgc acc acc ggc aag ctg ccc gtg	48
	Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val	
	1 5 10 15	
45	ccc tgg ccc acc ctc gtg acc acc ctc acc tgg ggc ctg cag tgc ttc	96
	Pro Trp Pro Thr Leu Val Thr Thr Leu Thr Trp Gly Leu Gln Cys Phe	
	20 25 30	
	gcc cgc tac ccc gac cac atg aag cgg cac gac ttc ttc aag tcc gcc	144
	Ala Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser Ala	
	35 40 45	
50	atg ccc gaa ggc tac gtc cag gag cgc acc atc ttc ttc aag gac gac	192
	Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp	
	50 55 60	
55	ggc aac tac aag acc cgc gcc gag gtg aag ttc gag ggc gac acc ctg	240
	Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu	
	65 70 75 80	

	gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag gac ggc aac	288
	Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn	
	85 90 95	
5	atc ctg ggg cac aag ctg gag tac aac tac atc agc cac aac gtc tat	336
	Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Ile Ser His Asn Val Tyr	
	100 105 110	
10	atc acc gcc gac aag cag aag aac ggc atc aag gtg aac ttc aag atc	384
	Ile Thr Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile	
	115 120 125	
15	cgc cac aac atc gag gac ggc agc gtg cag ctc gcc gac cac tac cag	432
	Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln	
	130 135 140	
20	cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc gac aac cac	480
	Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His	
	145 150 155 160	
	tac ctg agc acc cag tcc gcc ctg agc aaa gac ccc aac gag aag cgc	528
	Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg	
	165 170 175	
25	gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg atc act ctc	576
	Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr Leu	
	180 185 190	
30	ggc atg gac gag ctg tac aag	597
	Gly Met Asp Glu Leu Tyr Lys	
	195	
35	CFP F2A , F64L/S65T/Y66W/N146I/M153T mutations + Met @ pos. 1	
	SEQ ID NOS:98 & 99	
40	atg ggc aag ctg acc ctg aag ttc atc tgc acc acc ggc aag ctg ccc	48
	Met Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro	
	1 5 10 15	
45	gtg ccc tgg ccc acc ctc gtg acc acc ctc acc tgg ggc ctg cag tgc	96
	Val Pro Trp Pro Thr Leu Val Thr Thr Leu Thr Trp Gly Leu Gln Cys	
	20 25 30	
	ttc gcc cgc tac ccc gac cac atg aag cgg cac gac ttc ttc aag tcc	144
	Phe Ala Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser	
	35 40 45	
50	gcc atg ccc gaa ggc tac gtc cag gag cgc acc atc ttc ttc aag gac	192
	Ala Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp	
	50 55 60	
55	gac ggc aac tac aag acc cgc gcc gag gtg aag ttc gag ggc gac acc	240
	Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr	
	65 70 75 80	

	ctg gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag gac ggc	288
	Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly	
	85 90 95	
5	aac atc ctg ggg cac aag ctg gag tac aac tac atc agc cac aac gtc	336
	Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Ile Ser His Asn Val	
	100 105 110	
10	tat atc acc gcc gac aag cag aag aac ggc atc aag gtg aac ttc aag	384
	Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys	
	115 120 125	
15	atc cgc cac aac atc gag gac ggc agc gtg cag ctc gcc gac cac tac	432
	Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr	
	130 135 140	
20	cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc gac aac	480
	Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn	
	145 150 155 160	
	cac tac ctg agc acc cag tcc gcc ctg agc aaa gac ccc aac gag aag	528
	His Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys	
	165 170 175	
25	cgc gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg atc act	576
	Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr	
	180 185 190	
30	ctc ggc atg gac gag ctg tac aag	600
	Leu Gly Met Asp Glu Leu Tyr Lys	
	195 200	
35	CFP F2A, V163A mutation SEQ ID NOS:100 & 101	
40	ggc aag ctg acc ctg aag ttc atc tgc acc acc ggc aag ctg ccc gtg	48
	Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val	
	1 5 10 15	
45	ccc tgg ccc acc ctc gtg acc acc ttc ggc tac ggc ctg cag tgc ttc	96
	Pro Trp Pro Thr Leu Val Thr Thr Phe Gly Tyr Gly Leu Gln Cys Phe	
	20 25 30	
50	gcc cgc tac ccc gac cac atg aag cgg cac gac ttc ttc aag tcc gcc	144
	Ala Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser Ala	
	35 40 45	
	atg ccc gaa ggc tac gtc cag gag cgc acc atc ttc ttc aag gac gac	192
	Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp	
	50 55 60	
55	ggc aac tac aag acc cgc gcc gag gtg aag ttc gag ggc gac acc ctg	240
	Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu	
	65 70 75 80	

	gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag gac ggc aac	288
	Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn	
	85 90 95	
5	atc ctg ggg cac aag ctg gag tac aac tac aac agc cac aac gtc tat	336
	Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr	
	100 105 110	
10	atc atg gcc gac aag cag aag aac ggc atc aag gcc aac ttc aag atc	384
	Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Ala Asn Phe Lys Ile	
	115 120 125	
15	cgc cac aac atc gag gac ggc agc gtg cag ctc gcc gac cac tac cag	432
	Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln	
	130 135 140	
20	cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc gac aac cac	480
	Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His	
	145 150 155 160	
25	tac ctg agc acc cag tcc gcc ctg agc aaa gac ccc aac gag aag cgc	528
	Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg	
	165 170 175	
30	gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg atc act ctc	576
	Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr Leu	
	180 185 190	
35	ggc atg gac gag ctg tac aag	597
	Gly Met Asp Glu Leu Tyr Lys	
	195	
35	CFP F2A, V163A mutation + Met @ posit. 1	
	SEQ ID NOS:102 & 103	
40	atg ggc aag ctg acc ctg aag ttc atc tgc acc acc ggc aag ctg ccc	48
	Met Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro	
	1 5 10 15	
45	gtg ccc tgg ccc acc ctc gtg acc acc ttc ggc tac ggc ctg cag tgc	96
	Val Pro Trp Pro Thr Leu Val Thr Thr Phe Gly Tyr Gly Leu Gln Cys	
	20 25 30	
50	ttc gcc cgc tac ccc gac cac atg aag cgg cac gac ttc ttc aag tcc	144
	Phe Ala Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser	
	35 40 45	
55	gcc atg ccc gaa ggc tac gtc cag gag cgc acc atc ttc ttc aag gac	192
	Ala Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp	
	50 55 60	
60	gac ggc aac tac aag acc cgc gcc gag gtg aag ttc gag ggc gac acc	240
	Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr	
	65 70 75 80	

	ctg gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag gac ggc	288
	Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly	
	85 90 95	
5	aac atc ctg ggg cac aag ctg gag tac aac tac aac agc cac aac gtc	336
	Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val	
	100 105 110	
10	tat atc atg gcc gac aag cag aag aac ggc atc aag gcc aac ttc aag	384
	Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Ala Asn Phe Lys	
	115 120 125	
15	atc cgc cac aac atc gag gac ggc agc gtg cag ctc gcc gac cac tac	432
	Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr	
	130 135 140	
20	cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc gac aac	480
	Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn	
	145 150 155 160	
	cac tac ctg agc acc cag tcc gcc ctg agc aaa gac ccc aac gag aag	528
	His Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys	
	165 170 175	
25	cgc gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg atc act	576
	Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr	
	180 185 190	
30	ctc ggc atg gac gag ctg tac aag	600
	Leu Gly Met Asp Glu Leu Tyr Lys	
	195 200	
35	CFP F2A, N146I/ V163A mutations	
	SEQ ID NOS:104 & 105	
40	ggc aag ctg acc ctg aag ttc atc tgc acc acc ggc aag ctg ccc gtg	48
	Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val	
	1 5 10 15	
	ccc tgg ccc acc ctc gtg acc acc ttc ggc tac ggc ctg cag tgc ttc	96
	Pro Trp Pro Thr Leu Val Thr Thr Phe Gly Tyr Gly Leu Gln Cys Phe	
	20 25 30	
45	gcc cgc tac ccc gac cac atg aag cgg cac gac ttc ttc aag tcc gcc	144
	Ala Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser Ala	
	35 40 45	
50	atg ccc gaa ggc tac gtc cag gag cgc acc atc ttc ttc aag gac gac	192
	Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp	
	50 55 60	
55	ggc aac tac aag acc cgc gcc gag gtg aag ttc gag ggc gac acc ctg	240
	Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu	
	65 70 75 80	



	gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag gac ggc aac	288
	Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn	
	85 90 95	
5	atc ctg ggg cac aag ctg gag tac aac tac atc agc cac aac gtc tat	336
	Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Ile Ser His Asn Val Tyr	
	100 105 110	
10	atc atg gcc gac aag cag aag aac ggc atc aag gcc aac ttc aag atc	384
	Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Ala Asn Phe Lys Ile	
	115 120 125	
15	cgc cac aac atc gag gac ggc agc gtg cag ctc gcc gac cac tac cag	432
	Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln	
	130 135 140	
20	cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc gac aac cac	480
	Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His	
	145 150 155 160	
25	tac ctg agc acc cag tcc gcc ctg agc aaa gac ccc aac gag aag cgc	528
	Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg	
	165 170 175	
30	gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggc atc act ctc	576
	Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr Leu	
	180 185 190	
35	ggc atg gac gag ctg tac aag	597
	Gly Met Asp Glu Leu Tyr Lys	
	195	
40	CFP F2A, N146I/ V163A mutations + Met @ posit. 1	
	SEQ ID NOS:106 & 107	
40	atg ggc aag ctg acc ctg aag ttc atc tgc acc acc ggc aag ctg ccc	48
	Met Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro	
	1 5 10 15	
45	gtg ccc tgg ccc acc ctc gtg acc acc ttc ggc tac ggc ctg cag tgc	96
	Val Pro Trp Pro Thr Leu Val Thr Thr Phe Gly Tyr Gly Leu Gln Cys	
	20 25 30	
50	ttc gcc cgc tac ccc gac cac atg aag cgg cac gac ttc ttc aag tcc	144
	Phe Ala Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser	
	35 40 45	
55	gcc atg ccc gaa ggc tac gtc cag gag cgc acc atc ttc ttc aag gac	192
	Ala Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp	
	50 55 60	
60	gac ggc aac tac aag acc cgc gcc gag gtg aag ttc gag ggc gac acc	240
	Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr	
	65 70 75 80	

	ctg gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag gac ggc	288
	Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly	
	85 90 95	
5	aac atc ctg ggg cac aag ctg gag tac aac tac atc agc cac aac gtc	336
	Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Ile Ser His Asn Val	
	100 105 110	
10	tat atc atg gcc gac aag cag aag aac ggc atc aag gcc aac ttc aag	384
	Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Ala Asn Phe Lys	
	115 120 125	
15	atc cgc cac aac atc gag gac ggc agc gtg cag ctc gcc gac cac tac	432
	Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr	
	130 135 140	
20	cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc gac aac	480
	Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn	
	145 150 155 160	
	cac tac ctg agc acc cag tcc gcc ctg agc aaa gac ccc aac gag aag	528
	His Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys	
	165 170 175	
25	cgc gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg atc act	576
	Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr	
	180 185 190	
30	ctc ggc atg gac gag ctg tac aag	600
	Leu Gly Met Asp Glu Leu Tyr Lys	
	195 200	
35	CFP F2A, M153T/ V163A mutations	
	SEQ ID NOS:108 & 109	
40	ggc aag ctg acc ctg aag ttc atc tgc acc acc ggc aag ctg ccc gtg	48
	Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val	
	1 5 10 15	
	ccc tgg ccc acc ctc gtg acc acc ttc ggc tac ggc ctg cag tgc ttc	96
	Pro Trp Pro Thr Leu Val Thr Thr Phe Gly Tyr Gly Leu Gln Cys Phe	
	20 25 30	
45	gcc cgc tac ccc gac cac atg aag cgg cac gac ttc ttc aag tcc gcc	144
	Ala Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser Ala	
	35 40 45	
50	atg ccc gaa ggc tac gtc cag gag cgc acc atc ttc ttc aag gac gac	192
	Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp	
	50 55 60	
55	ggc aac tac aag acc cgc gcc gag gtg aag ttc gag ggc gac acc ctg	240
	Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu	
	65 70 75 80	

	gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag gac ggc aac	288
	Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn	
	85 90 95	
5	atc ctg ggg cac aag ctg gag tac aac tac aac agc cac aac gtc tat	336
	Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr	
	100 105 110	
10	atc acc gcc gac aag cag aag aac ggc atc aag gcc aac ttc aag atc	384
	Ile Thr Ala Asp Lys Gln Lys Asn Gly Ile Lys Ala Asn Phe Lys Ile	
	115 120 125	
15	cgc cac aac atc gag gac ggc agc gtg cag ctc gcc gac cac tac cag	432
	Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln	
	130 135 140	
20	cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc gac aac cac	480
	Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His	
	145 150 155 160	
25	tac ctg agc acc cag tcc gcc ctg agc aaa gac ccc aac gag aag cgc	528
	Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg	
	165 170 175	
30	gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg atc act ctc	576
	Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr Leu	
	180 185 190	
35	ggc atg gac gag ctg tac aag	597
	Gly Met Asp Glu Leu Tyr Lys	
	195	
40	CFP F2A, M153T/ V163A mutations + Met @ posit. 1	
	SEQ ID NOS:110 & 111	
40	atg ggc aag ctg acc ctg aag ttc atc tgc acc acc ggc aag ctg ccc	48
	Met Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro	
	1 5 10 15	
45	gtg ccc tgg ccc acc ctc gtg acc acc ttc ggc tac ggc ctg cag tgc	96
	Val Pro Trp Pro Thr Leu Val Thr Thr Phe Gly Tyr Gly Leu Gln Cys	
	20 25 30	
50	ttc gcc cgc tac ccc gac cac atg aag cgg cac gac ttc ttc aag tcc	144
	Phe Ala Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser	
	35 40 45	
55	gcc atg ccc gaa ggc tac gtc cag gag cgc acc atc ttc ttc aag gac	192
	Ala Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp	
	50 55 60	
60	gac ggc aac tac aag acc cgc gcc gag gtg aag ttc gag ggc gac acc	240
	Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr	
	65 70 75 80	

	ctg gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag gac ggc	288
	Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly	
	85 90 95	
5	aac atc ctg ggg cac aag ctg gag tac aac tac aac agc cac aac gtc	336
	Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val	
	100 105 110	
10	tat atc acc gcc gac aag cag aag aac ggc atc aag gcc aac ttc aag	384
	Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly Ile Lys Ala Asn Phe Lys	
	115 120 125	
15	atc cgc cac aac atc gag gac ggc agc gtg cag ctc gcc gac cac tac	432
	Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr	
	130 135 140	
20	cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc gac aac	480
	Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn	
	145 150 155 160	
	cac tac ctg agc acc cag tcc gcc ctg agc aaa gac ccc aac gag aag	528
	His Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys	
	165 170 175	
25	cgc gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg atc act	576
	Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr	
	180 185 190	
30	ctc ggc atg gac gag ctg tac aag	600
	Leu Gly Met Asp Glu Leu Tyr Lys	
	195 200	
35	CFP F2A, N146I/M153T/ V163A mutations	
	SEQ ID NOS:112 & 113	
40	ggc aag ctg acc ctg aag ttc atc tgc acc acc ggc aag ctg ccc gtg	48
	Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val	
	1 5 10 15	
	ccc tgg ccc acc ctc gtg acc acc ttc ggc tac ggc ctg cag tgc ttc	96
	Pro Trp Pro Thr Leu Val Thr Thr Phe Gly Tyr Gly Leu Gln Cys Phe	
	20 25 30	
45	gcc cgc tac ccc gac cac atg aag cgg cac gac ttc ttc aag tcc gcc	144
	Ala Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser Ala	
	35 40 45	
50	atg ccc gaa ggc tac gtc cag gag cgc acc atc ttc ttc aag gac gac	192
	Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp	
	50 55 60	
55	ggc aac tac aag acc cgc gcc gag gtg aag ttc gag ggc gac acc ctg	240
	Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu	
	65 70 75 80	

	gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag gac ggc aac	288
	Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn	
	85 90 95	
5	atc ctg ggg cac aag ctg gag tac aac tac atc agc cac aac gtc tat	336
	Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Ile Ser His Asn Val Tyr	
	100 105 110	
10	atc acc gcc gac aag cag aag aac ggc atc aag gcc aac ttc aag atc	384
	Ile Thr Ala Asp Lys Gln Lys Asn Gly Ile Lys Ala Asn Phe Lys Ile	
	115 120 125	
15	cgc cac aac atc gag gac ggc agc gtg cag ctc gcc gac cac tac cag	432
	Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln	
	130 135 140	
20	cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc gac aac cac	480
	Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His	
	145 150 155 160	
25	tac ctg agc acc cag tcc gcc ctg agc aaa gac ccc aac gag aag cgc	528
	Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg	
	165 170 175	
30	gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg atc act ctc	576
	Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr Leu	
	180 185 190	
35	ggc atg gac gag ctg tac aag	597
	Gly Met Asp Glu Leu Tyr Lys	
	195	
40	CFP F2A, N146I/M153T/ V163A mutations + Met @ pos.1	
	SEQ ID NOS:114 & 115	
40	atg ggc aag ctg acc ctg aag ttc atc tgc acc acc ggc aag ctg ccc	48
	Met Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro	
	1 5 10 15	
45	gtg ccc tgg ccc acc ctc gtg acc acc ttc ggc tac ggc ctg cag tgc	96
	Val Pro Trp Pro Thr Leu Val Thr Thr Phe Gly Tyr Gly Leu Gln Cys	
	20 25 30	
50	ttc gcc cgc tac ccc gac cac atg aag cgg cac gac ttc ttc aag tcc	144
	Phe Ala Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser	
	35 40 45	
55	gcc atg ccc gaa ggc tac gtc cag gag cgc acc atc ttc ttc aag gac	192
	Ala Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp	
	50 55 60	
60	gac ggc aac tac aag acc cgc gcc gag gtg aag ttc gag ggc gac acc	240
	Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr	
	65 70 75 80	

	ctg gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag gac ggc	288
	Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly	
	85 90 95	
5	aac atc ctg ggg cac aag ctg gag tac aac tac atc agc cac aac gtc	336
	Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Ile Ser His Asn Val	
	100 105 110	
10	tat atc acc gcc gac aag cag aag aac ggc atc aag gcc aac ttc aag	384
	Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly Ile Lys Ala Asn Phe Lys	
	115 120 125	
15	atc cgc cac aac atc gag gac ggc agc gtg cag ctc gcc gac cac tac	432
	Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr	
	130 135 140	
20	cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc gac aac	480
	Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn	
	145 150 155 160	
	cac tac ctg agc acc cag tcc gcc ctg agc aaa gac ccc aac gag aag	528
	His Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys	
	165 170 175	
25	cgc gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg atc act	576
	Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr	
	180 185 190	
30	ctc ggc atg gac gag ctg tac aag	600
	Leu Gly Met Asp Glu Leu Tyr Lys	
	195 200	
35	CGFP F2A ,F46L/S65T/Y66W/N146I/M153T/V163A/T203Y mutations SEQ ID NOS:116 & 117	
40	ggc aag ctg acc ctg aag ttc atc tgc acc acc ggc aag ctg ccc gtg	48
	Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val	
	1 5 10 15	
45	ccc tgg ccc acc ctc gtg acc acc ctg acc tgg ggc ctg cag tgc ttc	96
	Pro Trp Pro Thr Leu Val Thr Thr Leu Thr Trp Gly Leu Gln Cys Phe	
	20 25 30	
50	gcc cgc tac ccc gac cac atg aag cgg cac gac ttc ttc aag tcc gcc	144
	Ala Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser Ala	
	35 40 45	
	atg ccc gaa ggc tac gtc cag gag cgc acc atc ttc ttc aag gac gac	192
	Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp	
	50 55 60	
55	aac tac aag acc cgc gcc gag gtg aag ttc gag ggc gac acc ctg	240
	Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu	
	65 70 75 80	

	gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag gac ggc aac	288
	Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn	
	85 90 95	
5	atc ctg ggg cac aag ctg gag tac aac tac atc agc cac aac gtc tat	336
	Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Ile Ser His Asn Val Tyr	
	100 105 110	
10	atc acc gcc gac aag cag aag aac ggc atc aag gcc aac ttc aag atc	384
	Ile Thr Ala Asp Lys Gln Lys Asn Gly Ile Lys Ala Asn Phe Lys Ile	
	115 120 125	
15	cgc cac aac atc gag gac ggc agc gtg cag ctc gcc gac cac tac cag	432
	Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln	
	130 135 140	
20	cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc gac aac cac	480
	Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His	
	145 150 155 160	
25	tac ctg agc tac cag tcc gcc ctg agc aaa gac ccc aac gag aag cgc	528
	Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg	
	165 170 175	
30	gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg atc act ctc	576
	Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr Leu	
	180 185 190	
35	ggc atg gac gag ctg tac aag	597
	Gly Met Asp Glu Leu Tyr Lys	
	195	
35	CGFP F2A, F46L/S65T/Y66W/N146I/M153T/V163A/T203Y mutations + Met @ pos. 1	
	SEQ ID NOS:118 & 119	
40	atg ggc aag ctg acc ctg aag ttc atc tgc acc acc ggc aag ctg ccc	48
	Met Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro	
	1 5 10 15	
45	gtg ccc tgg ccc acc ctc gtg acc acc ctg acc tgg ggc ctg cag tgc	96
	Val Pro Trp Pro Thr Leu Val Thr Thr Leu Thr Trp Gly Leu Gln Cys	
	20 25 30	
50	ttc gcc cgc tac ccc gac cac atg aag cgg cac gac ttc ttc aag tcc	144
	Phe Ala Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser	
	35 40 45	
55	gcc atg ccc gaa ggc tac gtc cag gag cgc acc atc ttc ttc aag gac	192
	Ala Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp	
	50 55 60	
60	gac ggc aac tac aag acc cgc gcc gag gtg aag ttc gag ggc gac acc	240
	Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr	
	65 70 75 80	

	ctg gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag gac ggc	288
	Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly	
	85 90 95	
5	aac atc ctg ggg cac aag ctg gag tac aac tac atc agc cac aac gtc	336
	Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Ile Ser His Asn Val	
	100 105 110	
10	tat atc acc gcc gac aag cag aag aac ggc atc aag gcc aac ttc aag	384
	Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly Ile Lys Ala Asn Phe Lys	
	115 120 125	
15	atc cgc cac aac atc gag gac ggc agc gtg cag ctc gcc gac cac tac	432
	Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr	
	130 135 140	
20	cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc gac aac	480
	Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn	
	145 150 155 160	
	cac tac ctg agc tac cag tcc gcc ctg agc aaa gac ccc aac gag aag	528
	His Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys	
	165 170 175	
25	cgc gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg atc act	576
	Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr	
	180 185 190	
30	ctc ggc atg gac gag ctg tac aag	600
	Leu Gly Met Asp Glu Leu Tyr Lys	
	195 200	
35	CGFP F2A, N146I/T203Y mutations	
	SEQ ID NOS:120 & 121	
40	ggc aag ctg acc ctg aag ttc atc tgc acc acc ggc aag ctg ccc gtg	48
	Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val	
	1 5 10 15	
	ccc tgg ccc acc ctc gtg acc acc ttc ggc tac ggc ctg cag tgc ttc	96
	Pro Trp Pro Thr Leu Val Thr Thr Phe Gly Tyr Gly Leu Gln Cys Phe	
	20 25 30	
45	gcc cgc tac ccc gac cac atg aag cgg cac gac ttc ttc aag tcc gcc	144
	Ala Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser Ala	
	35 40 45	
50	atg ccc gaa ggc tac gtc cag gag cgc acc atc ttc ttc aag gac gac	192
	Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp	
	50 55 60	
55	ggc aac tac aag acc cgc gcc gag gtg aag ttc gag ggc gac acc ctg	240
	Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu	
	65 70 75 80	



	gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag gac ggc aac	288
	Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn	
	85 90 95	
5	atc ctg ggg cac aag ctg gag tac aac tac atc agc cac aac gtc tat	336
	Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Ile Ser His Asn Val Tyr	
	100 105 110	
10	atc atg gcc gac aag cag aag aac ggc atc aag gtg aac ttc aag atc	384
	Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile	
	115 120 125	
15	cgc cac aac atc gag gac ggc agc gtg cag ctc gcc gac cac tac cag	432
	Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln	
	130 135 140	
20	cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc gac aac cac	480
	Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His	
	145 150 155 160	
	tac ctg agc tac cag tcc gcc ctg agc aaa gac ccc aac gag aag cgc	528
	Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg	
	165 170 175	
25	gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg atc act ctc	576
	Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr Leu	
	180 185 190	
30	ggc atg gac gag ctg tac aag	597
	Gly Met Asp Glu Leu Tyr Lys	
	195	
35	CGFP F2A, N146I/T203Y mutations + Met @ posit. 1	
	SEQ ID NOS:122 & 123	
40	atg ggc aag ctg acc ctg aag ttc atc tgc acc acc ggc aag ctg ccc	48
	Met Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro	
	1 5 10 15	
	gtg ccc tgg ccc acc ctc gtg acc acc ttc ggc tac ggc ctg cag tgc	96
	Val Pro Trp Pro Thr Leu Val Thr Thr Phe Gly Tyr Gly Leu Gln Cys	
	20 25 30	
45	ttc gcc cgc tac ccc gac cac atg aag cgg cac gac ttc ttc aag tcc	144
	Phe Ala Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser	
	35 40 45	
50	gcc atg ccc gaa ggc tac gtc cag gag cgc acc atc ttc ttc aag gac	192
	Ala Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp	
	50 55 60	
55	gac ggc aac tac aag acc cgc gcc gag gtg aag ttc gag ggc gac acc	240
	Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr	
	65 70 75 80	

	ctg gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag gac ggc	288
	Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly	
	85 90 95	
5	aac atc ctg ggg cac aag ctg gag tac aac tac atc agc cac aac gtc	336
	Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Ile Ser His Asn Val	
	100 105 110	
10	tat atc atg gcc gac aag cag aag aac ggc atc aag gtg aac ttc aag	384
	Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys	
	115 120 125	
15	atc cgc cac aac atc gag gac ggc agc gtg cag ctc gcc gac cac tac	432
	Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr	
	130 135 140	
20	cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc gac aac	480
	Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn	
	145 150 155 160	
	cac tac ctg agc tac cag tcc gcc ctg agc aaa gac ccc aac gag aag	528
	His Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys	
	165 170 175	
25	cgc gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg atc act	576
	Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr	
	180 185 190	
30	ctc ggc atg gac gag ctg tac aag	600
	Leu Gly Met Asp Glu Leu Tyr Lys	
	195 200	
35	CGFP F2A, M153T/T203Y mutations	
	SEQ ID NOS:124 & 125	
40	ggc aag ctg acc ctg aag ttc atc tgc acc acc ggc aag ctg ccc gtg	48
	Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val	
	1 5 10 15	
	ccc tgg ccc acc ctc gtg acc acc ttc ggc tac ggc ctg cag tgc ttc	96
	Pro Trp Pro Thr Leu Val Thr Thr Phe Gly Tyr Gly Leu Gln Cys Phe	
	20 25 30	
45	gcc cgc tac ccc gac cac atg aag cgg cac gac ttc ttc aag tcc gcc	144
	Ala Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser Ala	
	35 40 45	
50	atg ccc gaa ggc tac gtc cag gag cgc acc atc ttc ttc aag gac gac	192
	Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp	
	50 55 60	
55	ggc aac tac aag acc cgc gcc gag gtg aag ttc gag ggc gac acc ctg	240
	Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu	
	65 70 75 80	

	gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag gac ggc aac	288
	Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn	
	85 90 95	
5	atc ctg ggg cac aag ctg gag tac aac tac aac agc cac aac gtc tat	336
	Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr	
	100 105 110	
10	atc acc gcc gac aag cag aag aac ggc atc aag gtg aac ttc aag atc	384
	Ile Thr Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile	
	115 120 125	
15	cgc cac aac atc gag gac ggc agc gtg cag ctc gcc gac cac tac cag	432
	Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln	
	130 135 140	
20	cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc gac aac cac	480
	Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His	
	145 150 155 160	
25	tac ctg agc tac cag tcc gcc ctg agc aaa gac ccc aac gag aag cgc	528
	Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg	
	165 170 175	
30	gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg atc act ctc	576
	Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr Leu	
	180 185 190	
35	ggc atg gac gag ctg tac aag	597
	Gly Met Asp Glu Leu Tyr Lys	
	195	
40	CGFP F2A, M153T/T203Y mutations + Met @ posit. 1	
	SEQ ID NOS:126 & 127	
45	atg ggc aag ctg acc ctg aag ttc atc tgc acc acc ggc aag ctg ccc	48
	Met Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro	
	1 5 10 15	
50	gtg ccc tgg ccc acc ctc gtg acc acc ttc ggc tac ggc ctg cag tgc	96
	Val Pro Trp Pro Thr Leu Val Thr Thr Phe Gly Tyr Gly Leu Gln Cys	
	20 25 30	
55	ttc gcc cgc tac ccc gac cac atg aag cgg cac gac ttc ttc aag tcc	144
	Phe Ala Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser	
	35 40 45	
60	gcc atg ccc gaa ggc tac gtc cag gag cgc acc atc ttc ttc aag gac	192
	Ala Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp	
	50 55 60	
65	gac ggc aac tac aag acc cgc gcc gag gtg aag ttc gag ggc gac acc	240
	Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr	
	65 70 75 80	

	ctg gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag gac ggc	288
	Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly	
	85 90 95	
5	aac atc ctg ggg cac aag ctg gag tac aac tac aac agc cac aac gtc	336
	Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val	
	100 105 110	
10	tat atc acc gcc gac aag cag aag aac ggc atc aag gtg aac ttc aag	384
	Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys	
	115 120 125	
15	atc cgc cac aac atc gag gac ggc agc gtg cag ctc gcc gac cac tac	432
	Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr	
	130 135 140	
20	cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc gac aac	480
	Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn	
	145 150 155 160	
	cac tac ctg agc tac cag tcc gcc ctg agc aaa gac ccc aac gag aag	528
	His Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys	
	165 170 175	
25	cgc gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg atc act	576
	Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr	
	180 185 190	
30	ctc ggc atg gac gag ctg tac aag	600
	Leu Gly Met Asp Glu Leu Tyr Lys	
	195 200	
35	CGFP F2A,N146I/ M153T/T203Y mutations	
	SEQ ID NOS:128 & 129	
40	ggc aag ctg acc ctg aag ttc atc tgc acc acc ggc aag ctg ccc gtg	48
	Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val	
	1 5 10 15	
45	ccc tgg ccc acc ctc gtg acc acc ttc ggc tac ggc ctg cag tgc ttc	96
	Pro Trp Pro Thr Leu Val Thr Thr Phe Gly Tyr Gly Leu Gln Cys Phe	
	20 25 30	
	gcc cgc tac ccc gac cac atg aag cgg cac gac ttc ttc aag tcc gcc	144
	Ala Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser Ala	
	35 40 45	
50	atg ccc gaa ggc tac gtc cag gag cgc acc atc ttc ttc aag gac gac	192
	Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp	
	50 55 60	
55	ggc aac tac aag acc cgc gcc gag gtg aag ttc gag ggc gac acc ctg	240
	Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu	
	65 70 75 80	

	gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag gac ggc aac	288
	Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn	
	85 90 95	
5	atc ctg ggg cac aag ctg gag tac aac tac atc agc cac aac gtc tat	336
	Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Ile Ser His Asn Val Tyr	
	100 105 110	
10	atc acc gcc gac aag cag aag aac ggc atc aag gtg aac ttc aag atc	384
	Ile Thr Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile	
	115 120 125	
15	cgc cac aac atc gag gac ggc agc gtg cag ctc gcc gac cac tac cag	432
	Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln	
	130 135 140	
20	cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc gac aac cac	480
	Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His	
	145 150 155 160	
25	tac ctg agc tac cag tcc gcc ctg agc aaa gac ccc aac gag aag cgc	528
	Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg	
	165 170 175	
30	gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg atc act ctc	576
	Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr Leu	
	180 185 190	
35	ggc atg gac gag ctg tac aag	597
	Gly Met Asp Glu Leu Tyr Lys	
	195	
35	CGFP F2A,N146I/ M153T/T203Y mutations + Met @ posit. 1	
	SEQ ID NOS:130 & 131	
40	atg ggc aag ctg acc ctg aag ttc atc tgc acc acc ggc aag ctg ccc	48
	Met Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro	
	1 5 10 15	
45	gtg ccc tgg ccc acc ctc gtg acc acc ttc ggc tac ggc ctg cag tgc	96
	Val Pro Trp Pro Thr Leu Val Thr Thr Phe Gly Tyr Gly Leu Gln Cys	
	20 25 30	
50	ttc gcc cgc tac ccc gac cac atg aag cgg cac gac ttc ttc aag tcc	144
	Phe Ala Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser	
	35 40 45	
55	gcc atg ccc gaa ggc tac gtc cag gag cgc acc atc ttc ttc aag gac	192
	Ala Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp	
	50 55 60	
60	gac ggc aac tac aag acc cgc gcc gag gtg aag ttc gag ggc gac acc	240
	Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr	
	65 70 75 80	

	ctg gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag gac ggc	288
	Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly	
	85 90 95	
5	aac atc ctg ggg cac aag ctg gag tac aac tac atc agc cac aac gtc	336
	Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Ile Ser His Asn Val	
	100 105 110	
10	tat atc acc gcc gac aag cag aag aac ggc atc aag gtg aac ttc aag	384
	Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys	
	115 120 125	
15	atc cgc cac aac atc gag gac ggc agc gtg cag ctc gcc gac cac tac	432
	Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr	
	130 135 140	
20	cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc gac aac	480
	Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn	
	145 150 155 160	
	cac tac ctg agc tac cag tcc gcc ctg agc aaa gac ccc aac gag aag	528
	His Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys	
	165 170 175	
25	cgc gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg atc act	576
	Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr	
	180 185 190	
30	ctc ggc atg gac gag ctg tac aag	600
	Leu Gly Met Asp Glu Leu Tyr Lys	
	195 200	
35	CGFP F2A, F64L/S65T/Y66W/N146I/M153T/T203Y mutations	
	SEQ ID NOS:132 & 133	
40	ggc aag ctg acc ctg aag ttc atc tgc acc acc ggc aag ctg ccc gtg	48
	Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val	
	1 5 10 15	
	ccc tgg ccc acc ctc gtg acc acc ctg acc tgg ggc ctg cag tgc ttc	96
	Pro Trp Pro Thr Leu Val Thr Thr Leu Thr Trp Gly Leu Gln Cys Phe	
	20 25 30	
45	gcc cgc tac ccc gac cac atg aag cgg cac gac ttc ttc aag tcc gcc	144
	Ala Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser Ala	
	35 40 45	
50	atg ccc gaa ggc tac gtc cag gag cgc acc atc ttc ttc aag gac gac	192
	Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp	
	50 55 60	
55	ggc aac tac aag acc cgc gcc gag gtg aag ttc gag ggc gac acc ctg	240
	Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu	
	65 70 75 80	

	gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag gac ggc aac	288
	Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn	
	85 90 95	
5	atc ctg ggg cac aag ctg gag tac aac tac atc agc cac aac gtc tat	336
	Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Ile Ser His Asn Val Tyr	
	100 105 110	
10	atc acc gcc gac aag cag aag aac ggc atc aag gtg aac ttc aag atc	384
	Ile Thr Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile	
	115 120 125	
15	cgc cac aac atc gag gac ggc agc gtg cag ctc gcc gac cac tac cag	432
	Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln	
	130 135 140	
20	cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc gac aac cac	480
	Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His	
	145 150 155 160	
25	tac ctg agc tac cag tcc gcc ctg agc aaa gac ccc aac gag aag cgc	528
	Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg	
	165 170 175	
30	gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggc atc act ctc	576
	Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr Leu	
	180 185 190	
35	ggc atg gac gag ctg tac aag	597
	Gly Met Asp Glu Leu Tyr Lys	
	195	
35	CGFP F2A F64L/S65T/Y66W/N146I/M153T/T203Y mutations + Met @ pos. 1 SEQ ID NOS:134 & 135	
40	atg ggc aag ctg acc ctg aag ttc atc tgc acc acc ggc aag ctg ccc	48
	Met Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro	
	1 5 10 15	
45	gtg ccc tgg ccc acc ctc gtg acc acc ctg acc tgg ggc ctg cag tgc	96
	Val Pro Trp Pro Thr Leu Val Thr Thr Leu Thr Trp Gly Leu Gln Cys	
	20 25 30	
50	ttc gcc cgc tac ccc gac cac atg aag cgg cac gac ttc ttc aag tcc	144
	Phe Ala Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser	
	35 40 45	
55	gcc atg ccc gaa ggc tac gtc cag gag cgc acc atc ttc ttc aag gac	192
	Ala Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp	
	50 55 60	
60	gac ggc aac tac aag acc cgc gcc gag gtg aag ttc gag ggc gac acc	240
	Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr	
	65 70 75 80	

	ctg gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag gac ggc Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly	288
	85 90 95	
5	aac atc ctg ggg cac aag ctg gag tac aac tac atc agc cac aac gtc Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Ile Ser His Asn Val	336
	100 105 110	
10	tat atc acc gcc gac aag cag aag aac ggc atc aag gtg aac ttc aag Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys	384
	115 120 125	
15	atc cgc cac aac atc gag gac ggc agc gtg cag ctc gcc gac cac tac Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr	432
	130 135 140	
20	cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc gac aac Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn	480
	145 150 155 160	
	cac tac ctg agc tac cag tcc gcc ctg agc aaa gac ccc aac gag aag His Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys	528
	165 170 175	
25	cgc gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg atc act Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr	576
	180 185 190	
30	ctc ggc atg gac gag ctg tac aag Leu Gly Met Asp Glu Leu Tyr Lys	600
	195 200	
35	CGFP F2A, V163A/T203Y mutations SEQ ID NOS:136 & 137	
40	ggc aag ctg acc ctg aag ttc atc tgc acc acc ggc aag ctg ccc gtg Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val	48
	1 5 10 15	
	ccc tgg ccc acc ctc gtg acc acc ttc ggc tac ggc ctg cag tgc ttc Pro Trp Pro Thr Leu Val Thr Thr Phe Gly Tyr Gly Leu Gln Cys Phe	96
	20 25 30	
45	gcc cgc tac ccc gac cac atg aag cgg cac gac ttc ttc aag tcc gcc Ala Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser Ala	144
	35 40 45	
50	atg ccc gaa ggc tac gtc cag gag cgc acc atc ttc ttc aag gac gac Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp	192
	50 55 60	
55	ggc aac tac aag acc cgc gcc gag gtg aag ttc gag ggc gac acc ctg Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu	240
	65 70 75 80	



	gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag gac ggc aac	288
	Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn	
	85 90 95	
5	atc ctg ggg cac aag ctg gag tac aac tac aac agc cac aac gtc tat	336
	Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr	
	100 105 110	
10	atc atg gcc gac aag cag aag aac ggc atc aag gcc aac ttc aag atc	384
	Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Ala Asn Phe Lys Ile	
	115 120 125	
15	cgc cac aac atc gag gac ggc agc gtg cag ctc gcc gac cac tac cag	432
	Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln	
	130 135 140	
20	cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc gac aac cac	480
	Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His	
	145 150 155 160	
	tac ctg agc tac cag tcc gcc ctg agc aaa gac ccc aac gag aag cgc	528
	Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg	
	165 170 175	
25	gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg atc act ctc	576
	Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr Leu	
	180 185 190	
30	ggc atg gac gag ctg tac aag	597
	Gly Met Asp Glu Leu Tyr Lys	
	195	
35	CGFP F2A, N146I/V163A/T203Y mutations	
	SEQ ID NOS:140 & 141	
40	ggc aag ctg acc ctg aag ttc atc tgc acc acc ggc aag ctg ccc gtg	48
	Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val	
	1 5 10 15	
	ccc tgg ccc acc ctc gtg acc acc ttc ggc tac ggc ctg cag tgc ttc	96
	Pro Trp Pro Thr Leu Val Thr Thr Phe Gly Tyr Gly Leu Gln Cys Phe	
	20 25 30	
45	gcc cgc tac ccc gac cac atg aag cgg cac gac ttc ttc aag tcc gcc	144
	Ala Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser Ala	
	35 40 45	
50	atg ccc gaa ggc tac gtc cag gag cgc acc atc ttc ttc aag gac gac	192
	Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp	
	50 55 60	
55	ggc aac tac aag acc cgc gcc gag gtg aag ttc gag ggc gac acc ctg	240
	Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu	
	65 70 75 80	

	gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag gac ggc aac	288
	Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn	
	85 90 95	
5	atc ctg ggg cac aag ctg gag tac aac tac atc agc cac aac gtc tat	336
	Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Ile Ser His Asn Val Tyr	
	100 105 110	
10	atc atg gcc gac aag cag aag aac ggc atc aag gcc aac ttc aag atc	384
	Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Ala Asn Phe Lys Ile	
	115 120 125	
15	cgc cac aac atc gag gac ggc agc gtg cag ctc gcc gac cac tac cag	432
	Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln	
	130 135 140	
20	cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc gac aac cac	480
	Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His	
	145 150 155 160	
25	tac ctg agc tac cag tcc gcc ctg agc aaa gac ccc aac gag aag cgc	528
	Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg	
	165 170 175	
30	gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg atc act ctc	576
	Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr Leu	
	180 185 190	
35	ggc atg gac gag ctg tac aag	597
	Gly Met Asp Glu Leu Tyr Lys	
	195	
40	CGFP F2A, N146I/V163A/T203Y mutations + Met @ pos. 1	
	SEQ ID NOS:142 & 143	
40	atg ggc aag ctg acc ctg aag ttc atc tgc acc acc ggc aag ctg ccc	48
	Met Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro	
	1 5 10 15	
45	gtg ccc tgg ccc acc ctc gtg acc acc ttc ggc tac ggc ctg cag tgc	96
	Val Pro Trp Pro Thr Leu Val Thr Thr Phe Gly Tyr Gly Leu Gln Cys	
	20 25 30	
50	ttc gcc cgc tac ccc gac cac atg aag cgg cac gac ttc ttc aag tcc	144
	Phe Ala Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser	
	35 40 45	
55	gcc atg ccc gaa ggc tac gtc cag gag cgc acc atc ttc ttc aag gac	192
	Ala Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp	
	50 55 60	
60	gac ggc aac tac aag acc cgc gcc gag gtg aag ttc gag ggc gac acc	240
	Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr	
	65 70 75 80	

	ctg gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag gac ggc	288
	Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly	
	85 90 95	
5	aac atc ctg ggg cac aag ctg gag tac aac tac atc agc cac aac gtc	336
	Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Ile Ser His Asn Val	
	100 105 110	
10	tat atc atg gcc gac aag cag aag aac ggc atc aag gcc aac ttc aag	384
	Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Ala Asn Phe Lys	
	115 120 125	
15	atc cgc cac aac atc gag gac ggc agc gtg cag ctc gcc gac cac tac	432
	Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr	
	130 135 140	
20	cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc gac aac	480
	Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn	
	145 150 155 160	
25	cac tac ctg agc tac cag tcc gcc ctg agc aaa gac ccc aac gag aag	528
	His Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys	
	165 170 175	
30	cgc gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg atc act	576
	Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr	
	180 185 190	
35	ctc ggc atg gac gag ctg tac aag	600
	Leu Gly Met Asp Glu Leu Tyr Lys	
	195 200	
35	CGFP F2A, M153T/V163A/T203Y mutations	
	SEQ ID NOS:144 & 145	
40	ggc aag ctg acc ctg aag ttc atc tgc acc acc ggc aag ctg ccc gtg	48
	Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val	
	1 5 10 15	
45	ccc tgg ccc acc ctc gtg acc acc ttc ggc tac ggc ctg cag tgc ttc	96
	Pro Trp Pro Thr Leu Val Thr Thr Phe Gly Tyr Gly Leu Gln Cys Phe	
	20 25 30	
50	ggc cgc tac ccc gac cac atg aag cgg cac gac ttc ttc aag tcc gcc	144
	Ala Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser Ala	
	35 40 45	
55	atg ccc gaa ggc tac gtc cag gag cgc acc atc ttc ttc aag gac gac	192
	Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp	
	50 55 60	
60	ggc aac tac aag acc cgc gcc gag gtg aag ttc gag ggc gac acc ctg	240
	Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu	
	65 70 75 80	

	gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag gac ggc aac	288
	Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn	
	85 90 95	
5	atc ctg ggg cac aag ctg gag tac aac tac aac agc cac aac gtc tat	336
	Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr	
	100 105 110	
10	atc acc gcc gac aag cag aag aac ggc atc aag gcc aac ttc aag atc	384
	Ile Thr Ala Asp Lys Gln Lys Asn Gly Ile Lys Ala Asn Phe Lys Ile	
	115 120 125	
15	cgc cac aac atc gag gac ggc agc gtg cag ctc gcc gac cac tac cag	432
	Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln	
	130 135 140	
20	cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc gac aac cac	480
	Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His	
	145 150 155 160	
	tac ctg agc tac cag tcc gcc ctg agc aaa gac ccc aac gag aag cgc	528
	Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg	
	165 170 175	
25	gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg atc act ctc	576
	Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr Leu	
	180 185 190	
30	ggc atg gac gag ctg tac aag	597
	Gly Met Asp Glu Leu Tyr Lys	
	195	
35	CGFP F2A, N146I/V163A/T203Y mutations + Met @ pos. 1	
	SEQ ID NOS:146 & 147	
40	atg ggc aag ctg acc ctg aag ttc atc tgc acc acc ggc aag ctg ccc	48
	Met Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro	
	1 5 10 15	
	gtg ccc tgg ccc acc ctc gtg acc acc ttc ggc tac ggc ctg cag tgc	96
	Val Pro Trp Pro Thr Leu Val Thr Thr Phe Gly Tyr Gly Leu Gln Cys	
	20 25 30	
45	ttc gcc cgc tac ccc gac cac atg aag cgg cac gac ttc ttc aag tcc	144
	Phe Ala Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser	
	35 40 45	
50	gcc atg ccc gaa ggc tac gtc cag gag cgc acc atc ttc ttc aag gac	192
	Ala Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp	
	50 55 60	
55	gac ggc aac tac aag acc cgc gcc gag gtg aag ttc gag ggc gac acc	240
	Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr	
	65 70 75 80	

	ctg gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag gac ggc	288
	Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly	
	85 90 95	
5	aac atc ctg ggg cac aag ctg gag tac aac tac aac agc cac aac gtc	336
	Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val	
	100 105 110	
10	tat atc acc gcc gac aag cag aag aac ggc atc aag gcc aac ttc aag	384
	Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly Ile Lys Ala Asn Phe Lys	
	115 120 125	
15	atc cgc cac aac atc gag gac ggc agc gtg cag ctc gcc gac cac tac	432
	Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr	
	130 135 140	
20	cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc gac aac	480
	Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn	
	145 150 155 160	
	cac tac ctg agc tac cag tcc gcc ctg agc aaa gac ccc aac gag aag	528
	His Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys	
	165 170 175	
25	cgc gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg atc act	576
	Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr	
	180 185 190	
30	ctc ggc atg gac gag ctg tac aag	600
	Leu Gly Met Asp Glu Leu Tyr Lys	
	195 200	
35	CGFP F2A, N146I/M153T/V163A/T203Y mutations	
	SEQ ID NOS:148 & 149	
40	ggc aag ctg acc ctg aag ttc atc tgc acc acc ggc aag ctg ccc gtg	48
	Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val	
	1 5 10 15	
45	ccc tgg ccc acc ctc gtg acc acc ttc ggc tac ggc ctg cag tgc ttc	96
	Pro Trp Pro Thr Leu Val Thr Thr Phe Gly Tyr Gly Leu Gln Cys Phe	
	20 25 30	
	gcc cgc tac ccc gac cac atg aag cgg cac gac ttc ttc aag tcc gcc	144
	Ala Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser Ala	
	35 40 45	
50	atg ccc gaa ggc tac gtc cag gag cgc acc atc ttc ttc aag gac gac	192
	Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp	
	50 55 60	
55	ggc aac tac aag acc cgc gcc gag gtg aag ttc gag ggc gac acc ctg	240
	Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu	
	65 70 75 80	

	gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag gac ggc aac	288
	Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn	
	85 90 95	
5	atc ctg ggg cac aag ctg gag tac aac tac atc agc cac aac gtc tat	336
	Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Ile Ser His Asn Val Tyr	
	100 105 110	
10	atc acc gcc gac aag cag aag aac ggc atc aag gcc aac ttc aag atc	384
	Ile Thr Ala Asp Lys Gln Lys Asn Gly Ile Lys Ala Asn Phe Lys Ile	
	115 120 125	
15	cgc cac aac atc gag gac ggc agc gtg cag ctc gcc gac cac tac cag	432
	Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln	
	130 135 140	
20	cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc gac aac cac	480
	Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His	
	145 150 155 160	
	tac ctg agc tac cag tcc gcc ctg agc aaa gac ccc aac gag aag cgc	528
	Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg	
	165 170 175	
25	gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg atc act ctc	576
	Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr Leu	
	180 185 190	
30	ggc atg gac gag ctg tac aag	597
	Gly Met Asp Glu Leu Tyr Lys	
	195	
35	CGFP F2A,N146I/M153T/V163A/T203Y mutations + Met @ posit: 1	
	SEQ ID NOS:150 & 151	
40	atg ggc aag ctg acc ctg aag ttc atc tgc acc acc ggc aag ctg ccc	48
	Met Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro	
	1 5 10 15	
	gtg ccc tgg ccc acc ctc gtg acc acc ttc ggc tac ggc ctg cag tgc	96
	Val Pro Trp Pro Thr Leu Val Thr Thr Phe Gly Tyr Gly Leu Gln Cys	
	20 25 30	
45	ttc gcc cgc tac ccc gac cac atg aag cgg cac gac ttc ttc aag tcc	144
	Phe Ala Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser	
	35 40 45	
50	gcc atg ccc gaa ggc tac gtc cag gag cgc acc atc ttc ttc aag gac	192
	Ala Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp	
	50 55 60	
55	gac ggc aac tac aag acc cgc gcc gag gtg aag ttc gag ggc gac acc	240
	Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr	
	65 70 75 80	

	ctg gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag gac ggc	288
	Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly	
	85 90 95	
5	aac atc ctg ggg cac aag ctg gag tac aac tac atc agc cac aac gtc	336
	Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Ile Ser His Asn Val	
	100 105 110	
10	tat atc acc gcc gac aag cag aag aac ggc atc aag gcc aac ttc aag	384
	Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly Ile Lys Ala Asn Phe Lys	
	115 120 125	
15	atc cgc cac aac atc gag gac ggc agc gtg cag ctc gcc gac cac tac	432
	Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr	
	130 135 140	
20	cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc gac aac	480
	Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn	
	145 150 155 160	
	cac tac ctg agc tac cag tcc gcc ctg agc aaa gac ccc aac gag aag	528
	His Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys	
	165 170 175	
25	cgc gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg atc act	576
	Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr	
	180 185 190	
30	ctc ggc atg gac gag ctg tac aag	600
	Leu Gly Met Asp Glu Leu Tyr Lys	
	195 200	
35	BFP F2A, Y66H mutation	
	SEQ ID NOS:152 & 153	
40	ggc aag ctg acc ctg aag ttc atc tgc acc acc ggc aag ctg ccc gtg	48
	Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val	
	1 5 10 15	
	ccc tgg ccc acc ctc gtg acc acc ttc ggc cac ggc ctg cag tgc ttc	96
	Pro Trp Pro Thr Leu Val Thr Thr Phe Gly His Gly Leu Gln Cys Phe	
	20 25 30	
45	gcc cgc tac ccc gac cac atg aag cgg cac gac ttc ttc aag tcc gcc	144
	Ala Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser Ala	
	35 40 45	
50	atg ccc gaa ggc tac gtc cag gag cgc acc atc ttc ttc aag gac gac	192
	Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp	
	50 55 60	
55	ggc aac tac aag acc cgc gcc gag gtg aag ttc gag ggc gac acc ctg	240
	Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu	
	65 70 75 80	

	gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag gac ggc aac	288
	Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn	
	85 90 95	
5	atc ctg ggg cac aag ctg gag tac aac tac aac agc cac aac gtc tat	336
	Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr	
	100 105 110	
10	atc atg gcc gac aag cag aag aac ggc atc aag gtg aac ttc aag atc	384
	Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile	
	115 120 125	
15	cgc cac aac atc gag gac ggc agc gtg cag ctc gcc gac cac tac cag	432
	Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln	
	130 135 140	
20	cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc gac aac cac	480
	Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His	
	145 150 155 160	
	tac ctg agc acc cag tcc gcc ctg agc aaa gac ccc aac gag aag cgc	528
	Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg	
	165 170 175	
25	gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg atc act ctc	576
	Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr Leu	
	180 185 190	
30	ggc atg gac gag ctg tac aag	597
	Gly Met Asp Glu Leu Tyr Lys	
	195	
35	BFP F2A, Y66H mutation + Met @ posit. 1	
	SEQ ID NOS:154 & 155	
40	atg ggc aag ctg acc ctg aag ttc atc tgc acc acc ggc aag ctg ccc	48
	Met Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro	
	1 5 10 15	
	gtg ccc tgg ccc acc ctc gtg acc acc ttc ggc cac ggc ctg cag tgc	96
	Val Pro Trp Pro Thr Leu Val Thr Thr Phe Gly His Gly Leu Gln Cys	
	20 25 30	
45	ttc gcc cgc tac ccc gac cac atg aag cgg cac gac ttc ttc aag tcc	144
	Phe Ala Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser	
	35 40 45	
50	gcc atg ccc gaa ggc tac gtc cag gag cgc acc atc ttc ttc aag gac	192
	Ala Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp	
	50 55 60	
55	gac ggc aac tac aag acc cgc gcc gag gtg aag ttc gag ggc gac acc	240
	Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr	
	65 70 75 80	



	ctg gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag gac ggc	288
	Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly	
	85 90 95	
5	aac atc ctg ggg cac aag ctg gag tac aac tac aac agc cac aac gtc	336
	Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val	
	100 105 110	
10	tat atc atg gcc gac aag cag aag aac ggc atc aag gtg aac ttc aag	384
	Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys	
	115 120 125	
15	atc cgc cac aac atc gag gac ggc agc gtg cag ctc gcc gac cac tac	432
	Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr	
	130 135 140	
20	cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc gac aac	480
	Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn	
	145 150 155 160	
25	cac tac ctg agc acc cag tcc gcc ctg agc aaa gac ccc aac gag aag	528
	His Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys	
	165 170 175	
30	ctc ggc atg gac gag ctg tac aag	600
	Leu Gly Met Asp Glu Leu Tyr Lys	
	195 200	
35	BFP F2A, Y145F mutation	
	SEQ ID NOS:156 & 157	
40	ggc aag ctg acc ctg aag ttc atc tgc acc acc ggc aag ctg ccc gtg	48
	Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val	
	1 5 10 15	
45	ccc tgg ccc acc ctc gtg acc acc ttc ggc tac ggc ctg cag tgc ttc	96
	Pro Trp Pro Thr Leu Val Thr Thr Phe Gly Tyr Gly Leu Gln Cys Phe	
	20 25 30	
50	gcc cgc tac ccc gac cac atg aag cgg cac gac ttc ttc aag tcc gcc	144
	Ala Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser Ala	
	35 40 45	
55	atg ccc gaa ggc tac gtc cag gag cgc acc atc ttc ttc aag gac gac	192
	Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp	
	50 55 60	
60	ggc aac tac aag acc cgc gcc gag gtg aag ttc gag ggc gac acc ctg	240
	Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu	
	65 70 75 80	

	gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag gac ggc aac	288
	Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn	
	85 90 95	
5	atc ctg ggg cac aag ctg gag tac aac ttc aac agc cac aac gtc tat	336
	Ile Leu Gly His Lys Leu Glu Tyr Asn Phe Asn Ser His Asn Val Tyr	
	100 105 110	
10	atc atg gcc gac aag cag aag aac ggc atc aag gtg aac ttc aag atc	384
	Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile	
	115 120 125	
15	cgc cac aac atc gag gac ggc agc gtg cag ctc gcc gac cac tac cag	432
	Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln	
	130 135 140	
20	cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc gac aac cac	480
	Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His	
	145 150 155 160	
25	tac ctg agc tac cag tcc gcc ctg agc aaa gac ccc aac gag aag cgc	528
	Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg	
	165 170 175	
30	gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg atc act ctc	576
	Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr Leu	
	180 185 190	
35	ggc atg gac gag ctg tac aag	597
	Gly Met Asp Glu Leu Tyr Lys	
	195	
40	BFP F2A, Y145F mutation + Met @ position 1	
	SEQ ID NOS:158 & 159	
40	atg ggc aag ctg acc ctg aag ttc atc tgc acc acc ggc aag ctg ccc	48
	Met Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro	
	1 5 10 15	
45	gtg ccc tgg ccc acc ctc gtg acc acc ttc ggc tac ggc ctg cag tgc	96
	Val Pro Trp Pro Thr Leu Val Thr Thr Phe Gly Tyr Gly Leu Gln Cys	
	20 25 30	
50	ttc gcc cgc tac ccc gac cac atg aag cgg cac gac ttc ttc aag tcc	144
	Phe Ala Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser	
	35 40 45	
55	gcc atg ccc gaa ggc tac gtc cag gag cgc acc atc ttc ttc aag gac	192
	Ala Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp	
	50 55 60	
60	gac ggc aac tac aag acc cgc gcc gag gtg aag ttc gag ggc gac acc	240
	Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr	
	65 70 75 80	

	ctg gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag gac ggc	288
	Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly	
	85 90 95	
5	aac atc ctg ggg cac aag ctg gag tac aac ttc aac agc cac aac gtc	336
	Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Phe Asn Ser His Asn Val	
	100 105 110	
10	tat atc atg gcc gac aag cag aag aac ggc atc aag gtg aac ttc aag	384
	Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys	
	115 120 125	
15	atc cgc cac aac atc gag gac ggc agc gtg cag ctc gcc gac cac tac	432
	Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr	
	130 135 140	
20	cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc gac aac	480
	Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn	
	145 150 155 160	
	cac tac ctg agc tac cag tcc gcc ctg agc aaa gac ccc aac gag aag	528
	His Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys	
	165 170 175	
25	cgc gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg atc act	576
	Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr	
	180 185 190	
30	ctc ggc atg gac gag ctg tac aag	600
	Leu Gly Met Asp Glu Leu Tyr Lys	
	195 200	
35	BFP F2A, Y66H/Y145F mutations	
	SEQ ID NOS:160 & 161	
40	ggc aag ctg acc ctg aag ttc atc tgc acc acc ggc aag ctg ccc gtg	48
	Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val	
	1 5 10 15	
45	ccc tgg ccc acc ctc gtg acc acc ttc ggc cac ggc ctg cag tgc ttc	96
	Pro Trp Pro Thr Leu Val Thr Thr Phe Gly His Gly Leu Gln Cys Phe	
	20 25 30	
	gcc cgc tac ccc gac cac atg aag cgg cac gac ttc ttc aag tcc gcc	144
	Ala Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser Ala	
	35 40 45	
50	atg ccc gaa ggc tac gtc cag gag cgc acc atc ttc ttc aag gac gac	192
	Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp	
	50 55 60	
55	ggc aac tac aag acc cgc gcc gag gtg aag ttc gag ggc gac acc ctg	240
	Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu	
	65 70 75 80	

	gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag gac ggc aac	288
	Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn	
	85 90 95	
5	atc ctg ggg cac aag ctg gag tac aac ttc aac agc cac aac gtc tat	336
	Ile Leu Gly His Lys Leu Glu Tyr Asn Phe Asn Ser His Asn Val Tyr	
	100 105 110	
10	atc atg gcc gac aag cag aag aac ggc atc aag gtg aac ttc aag atc	384
	Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile	
	115 120 125	
15	cgc cac aac atc gag gac ggc agc gtg cag ctc gcc gac cac tac cag	432
	Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln	
	130 135 140	
20	cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc gac aac cac	480
	Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His	
	145 150 155 160	
25	tac ctg agc acc cag tcc gcc ctg agc aaa gac ccc aac gag aag cgc	528
	Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg	
	165 170 175	
30	gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg atc act ctc	576
	Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr Leu	
	180 185 190	
35	ggc atg gac gag ctg tac aag	597
	Gly Met Asp Glu Leu Tyr Lys	
	195	
40	BFP F2A, Y66H/Y145F mutations + Met @ pos. 1	
	SEQ ID NOS:162 & 163	
40	atg ggc aag ctg acc ctg aag ttc atc tgc acc acc ggc aag ctg ccc	48
	Met Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro	
	1 5 10 15	
45	gtg ccc tgg ccc acc ctc gtg acc acc ttc ggc cac ggc ctg cag tgc	96
	Val Pro Trp Pro Thr Leu Val Thr Thr Phe Gly His Gly Leu Gln Cys	
	20 25 30	
50	ttc gcc cgc tac ccc gac cac atg aag cgg cac gac ttc ttc aag tcc	144
	Phe Ala Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser	
	35 40 45	
55	gcc atg ccc gaa ggc tac gtc cag gag cgc acc atc ttc ttc aag gac	192
	Ala Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp	
	50 55 60	
60	gac ggc aac tac aag acc cgc gcc gag gtg aag ttc gag ggc gac acc	240
	Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr	
	65 70 75 80	

	ctg gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag gac ggc	288
	Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly	
	85 90 95	
5	aac atc ctg ggg cac aag ctg gag tac aac ttc aac agc cac aac gtc	336
	Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Phe Asn Ser His Asn Val	
	100 105 110	
10	tat atc atg gcc gac aag cag aag aac ggc atc aag gtg aac ttc aag	384
	Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys	
	115 120 125	
15	atc cgc cac aac atc gag gac ggc agc gtg cag ctc gcc gac cac tac	432
	Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr	
	130 135 140	
20	cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc gac aac	480
	Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn	
	145 150 155 160	
	cac tac ctg agc acc cag tcc gcc ctg agc aaa gac ccc aac gag aag	528
	His Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys	
	165 170 175	
25	cgc gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg atc act	576
	Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr	
	180 185 190	
30	ctc ggc atg gac gag ctg tac aag	600
	Leu Gly Met Asp Glu Leu Tyr Lys	
	195 200	
35	BFP F2A, F64L/Y66H/Y145F mutations	
	SEQ ID NOS:164 & 165	
40	ggc aag ctg acc ctg aag ttc atc tgc acc acc ggc aag ctg ccc gtg	48
	Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val	
	1 5 10 15	
	ccc tgg ccc acc ctc gtg acc acc ctg ggc cac ggc ctg cag tgc ttc	96
	Pro Trp Pro Thr Leu Val Thr Thr Leu Gly His Gly Leu Gln Cys Phe	
	20 25 30	
45	gcc cgc tac ccc gac cac atg aag cgg cac gac ttc ttc aag tcc gcc	144
	Ala Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser Ala	
	35 40 45	
50	atg ccc gaa ggc tac gtc cag gag cgc acc atc ttc ttc aag gac gac	192
	Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp	
	50 55 60	
55	ggc aac tac aag acc cgc gcc gag gtg aag ttc gag ggc gac acc ctg	240
	Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu	
	65 70 75 80	

	gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag gac ggc aac	288
	Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn	
	85 90 95	
5	atc ctg ggg cac aag ctg gag tac aac ttc aac agc cac aac gtc tat	336
	Ile Leu Gly His Lys Leu Glu Tyr Asn Phe Asn Ser His Asn Val Tyr	
	100 105 110	
10	atc atg gcc gac aag cag aag aac ggc atc aag gtg aac ttc aag atc	384
	Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile	
	115 120 125	
15	cgc cac aac atc gag gac ggc agc gtg cag ctc gcc gac cac tac cag	432
	Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln	
	130 135 140	
20	cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc gac aac cac	480
	Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His	
	145 150 155 160	
	tac ctg agc acc cag tcc gcc ctg agc aaa gac ccc aac gag aag cgc	528
	Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg	
	165 170 175	
25	gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg atc act ctc	576
	Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr Leu	
	180 185 190	
30	ggc atg gac gag ctg tac aag	597
	Gly Met Asp Glu Leu Tyr Lys	
	195	
35	BFP F2A, F64L/Y66H/Y145F mutations + Met @ posit. 1	
	SEQ ID NOS:166 & 167	
40	atg ggc aag ctg acc ctg aag ttc atc tgc acc acc ggc aag ctg ccc	48
	Met Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro	
	1 5 10 15	
45	gtg ccc tgg ccc acc ctc gtg acc acc ctg ggc cac ggc ctg cag tgc	96
	Val Pro Trp Pro Thr Leu Val Thr Thr Leu Gly His Gly Leu Gln Cys	
	20 25 30	
	ttc gcc cgc tac ccc gac cac atg aag cgg cac gac ttc ttc aag tcc	144
	Phe Ala Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser	
	35 40 45	
50	gcc atg ccc gaa ggc tac gtc cag gag cgc acc atc ttc ttc aag gac	192
	Ala Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp	
	50 55 60	
55	gac ggc aac tac aag acc cgc gcc gag gtg aag ttc gag ggc gac acc	240
	Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr	
	65 70 75 80	

	ctg gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag gac ggc	288
	Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly	
	85 90 95	
5	aac atc ctg ggg cac aag ctg gag tac aac ttc aac agc cac aac gtc	336
	Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Phe Asn Ser His Asn Val	
	100 105 110	
10	tat atc atg gcc gac aag cag aag aac ggc atc aag gtg aac ttc aag	384
	Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys	
	115 120 125	
15	atc cgc cac aac atc gag gac ggc agc gtg cag ctc gcc gac cac tac	432
	Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr	
	130 135 140	
20	cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc gac aac	480
	Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn	
	145 150 155 160	
	cac tac ctg agc acc cag tcc gcc ctg agc aaa gac ccc aac gag aag	528
	His Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys	
	165 170 175	
25	cgc gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg atc act	576
	Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr	
	180 185 190	
30	ctc ggc atg gac gag ctg tac aag	600
	Leu Gly Met Asp Glu Leu Tyr Lys	
	195 200	
35	EGFP F2A + Met @ posit. 1	
	SEQ ID NOS:168 & 169	
40	atg ggc aag ctg acc ctg aag ttc atc tgc acc acc ggc aag ctg ccc	48
	Met Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro	
	1 5 10 15	
	gtg ccc tgg ccc acc ctc gtg acc acc ctg acc tac ggc gtg cag tgc	96
	Val Pro Trp Pro Thr Leu Val Thr Thr Leu Thr Tyr Gly Val Gln Cys	
	20 25 30	
45	ttc tcc cgc tac ccc gac cac atg aag cgg cac gac ttc ttc aag tcc	144
	Phe Ser Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser	
	35 40 45	
50	gcc atg ccc gaa ggc tac gtc cag gag cgc acc atc ttc ttc aag gac	192
	Ala Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp	
	50 55 60	
55	gac ggc aac tac aag acc cgc gcc gag gtg aag ttc gag ggc gac acc	240
	Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr	
	65 70 75 80	

	ctg gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag gac ggc	288
	Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly	
	85 90 95	
5	aac atc ctg ggg cac aag ctg gag tac aac tac aac agc cac aac gtc	336
	Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val	
	100 105 110	
10	tat atc atg gcc gac aag cag aag aac ggc atc aag gtg aac ttc aag	384
	Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys	
	115 120 125	
15	atc cgc cac aac atc gag gac ggc agc gtg cag ctc gcc gac cac tac	432
	Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr	
	130 135 140	
20	cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc gac aac	480
	Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn	
	145 150 155 160	
	cac tac ctg agc tac cag tcc gcc ctg agc aaa gac ccc aac gag aag	528
	His Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys	
	165 170 175	
25	cgc gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg atc act	576
	Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr	
	180 185 190	
30	ctc ggc atg gac gag ctg tac aag	600
	Leu Gly Met Asp Glu Leu Tyr Lys	
	195 200	
35	EGFP emerald F2A, S65T/S72A/N149K/M153T/I167T mutations	
	SEQ ID NOS:170 & 171	
40	ggc aag ctg acc ctg aag ttc atc tgc acc acc ggc aag ctg ccc gtg	48
	Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val	
	1 5 10 15	
	ccc tgg ccc acc ctc gtg acc acc ttc acc tac ggc ctg cag tgc ttc	96
	Pro Trp Pro Thr Leu Val Thr Thr Phe Thr Tyr Gly Leu Gln Cys Phe	
	20 25 30	
45	gcc cgc tac ccc gac cac atg aag cgg cac gac ttc ttc aag tcc gcc	144
	Ala Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser Ala	
	35 40 45	
50	atg ccc gaa ggc tac gtc cag gag cgc acc atc ttc ttc aag gac gac	192
	Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp	
	50 55 60	
55	ggc aac tac aag acc cgc gcc gag gtg aag ttc gag ggc gac acc ctg	240
	Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu	
	65 70 75 80	



	gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag gac ggc aac	288
	Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn	
	85 90 95	
5	atc ctg ggg cac aag ctg gag tac aac tac aac agc cac aag gtc tat	336
	Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Lys Val Tyr	
	100 105 110	
10	atc acc gcc gac aag cag aag aac ggc atc aag gtg aac ttc aag acc	384
	Ile Thr Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Thr	
	115 120 125	
15	cgc cac aac atc gag gac ggc agc gtg cag ctc gcc gac cac tac cag	432
	Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln	
	130 135 140	
20	cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc gac aac cac	480
	Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His	
	145 150 155 160	
25	tac ctg agc tac cag tcc gcc ctg agc aaa gac ccc aac gag aag cgc	528
	Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg	
	165 170 175	
30	gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg atc act ctc	576
	Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr Leu	
	180 185 190	
35	ggc atg gac gag ctg tac aag	597
	Gly Met Asp Glu Leu Tyr Lys	
	195	
40	EGFP emerald F2A, S65T/S72A/N149K/M153T/I167T mutations + Met @ pos. 1 SEQ ID NOS:172 & 173	
40	atg ggc aag ctg acc ctg aag ttc atc tgc acc acc ggc aag ctg ccc	48
	Met Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro	
	1 5 10 15	
45	gtg ccc tgg ccc acc ctc gtg acc acc ttc acc tac ggc ctg cag tgc	96
	Val Pro Trp Pro Thr Leu Val Thr Thr Phe Thr Tyr Gly Leu Gln Cys	
	20 25 30	
50	ttc gcc cgc tac ccc gac cac atg aag cgg cac gac ttc ttc aag tcc	144
	Phe Ala Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser	
	35 40 45	
55	gcc atg ccc gaa ggc tac gtc cag gag cgc acc atc ttc ttc aag gac	192
	Ala Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp	
	50 55 60	
60	gac ggc aac tac aag acc cgc gcc gag gtg aag ttc gag ggc gac acc	240
	Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr	
	65 70 75 80	

	ctg gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag gac ggc	288
	Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly	
	85 90 95	
5	aac atc ctg ggg cac aag ctg gag tac aac tac aac agc cac aag gtc	336
	Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Lys Val	
	100 105 110	
10	tat atc acc gcc gac aag cag aag aac ggc atc aag gtg aac ttc aag	384
	Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys	
	115 120 125	
15	acc cgc cac aac atc gag gac ggc agc gtg cag ctc gcc gac cac tac	432
	Thr Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr	
	130 135 140	
20	cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc gac aac	480
	Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn	
	145 150 155 160	
	cac tac ctg agc tac cag tcc gcc ctg agc aaa gac ccc aac gag aag	528
	His Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys	
	165 170 175	
25	cgc gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg atc act	576
	Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr	
	180 185 190	
30	ctc ggc atg gac gag ctg tac aag	600
	Leu Gly Met Asp Glu Leu Tyr Lys	
	195 200	
35	YFP F2A, Y203F mutation	
	SEQ ID NOS:174 & 175	
40	ggc aag ctg acc ctg aag ttc atc tgc acc acc ggc aag ctg ccc gtg	48
	Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val	
	1 5 10 15	
	ccc tgg ccc acc ctc gtg acc acc ttc ggc tac ggc ctg cag tgc ttc	96
	Pro Trp Pro Thr Leu Val Thr Thr Phe Gly Tyr Gly Leu Gln Cys Phe	
	20 25 30	
45	gcc cgc tac ccc gac cac atg aag cgg cac gac ttc ttc aag tcc gcc	144
	Ala Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser Ala	
	35 40 45	
50	atg ccc gaa ggc tac gtc cag gag cgc acc atc ttc ttc aag gac gac	192
	Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp	
	50 55 60	
55	ggc aac tac aag acc cgc gcc gag gtg aag ttc gag ggc gac acc ctg	240
	Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu	
	65 70 75 80	

	gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag gac ggc aac	288
	Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn	
	85 90 95	
5	atc ctg ggg cac aag ctg gag tac aac tac aac agc cac aac gtc tat	336
	Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr	
	100 105 110	
10	atc atg gcc gac aag cag aag aac ggc atc aag gtg aac ttc aag atc	384
	Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile	
	115 120 125	
15	cgc cac aac atc gag gac ggc agc gtg cag ctc gcc gac cac tac cag	432
	Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln	
	130 135 140	
20	cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc gac aac cac	480
	Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His	
	145 150 155 160	
25	tac ctg agc ttc cag tcc gcc ctg agc aaa gac ccc aac gag aag cgc	528
	Tyr Leu Ser Phe Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg	
	165 170 175	
30	gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg atc act ctc	576
	Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr Leu	
	180 185 190	
35	ggc atg gac gag ctg tac aag	597
	Gly Met Asp Glu Leu Tyr Lys	
	195	
40	YFP F2A, Y203F mutation + Met @ pos. 1	
	SEQ ID NOS:176 & 177	
40	atg ggc aag ctg acc ctg aag ttc atc tgc acc acc ggc aag ctg ccc	48
	Met Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro	
	1 5 10 15	
45	gtg ccc tgg ccc acc ctc gtg acc acc ttc ggc tac ggc ctg cag tgc	96
	Val Pro Trp Pro Thr Leu Val Thr Thr Phe Gly Tyr Gly Leu Gln Cys	
	20 25 30	
50	ttc gcc cgc tac ccc gac cac atg aag cgg cac gac ttc ttc aag tcc	144
	Phe Ala Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser	
	35 40 45	
55	gcc atg ccc gaa ggc tac gtc cag gag cgc acc atc ttc ttc aag gac	192
	Ala Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp	
	50 55 60	
60	gac ggc aac tac aag acc cgc gcc gag gtg aag ttc gag ggc gac acc	240
	Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr	
	65 70 75 80	

	ctg gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag gac ggc	288
	Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly	
	85 90 95	
5	aac atc ctg ggg cac aag ctg gag tac aac tac aac agc cac aac gtc	336
	Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val	
	100 105 110	
10	tat atc atg gcc gac aag cag aag aac ggc atc aag gtg aac ttc aag	384
	Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys	
	115 120 125	
15	atc cgc cac aac atc gag gac ggc agc gtg cag ctc gcc gac cac tac	432
	Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr	
	130 135 140	
20	cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc gac aac	480
	Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn	
	145 150 155 160	
	cac tac ctg agc ttc cag tcc gcc ctg agc aaa gac ccc aac gag aag	528
	His Tyr Leu Ser Phe Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys	
	165 170 175	
25	cgc gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg atc act	576
	Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr	
	180 185 190	
30	ctc ggc atg gac gag ctg tac aag	600
	Leu Gly Met Asp Glu Leu Tyr Lys	
	195 200	
35	YFP F2A, Y203H mutation SEQ ID NOS:178 & 179	
40	ggc aag ctg acc ctg aag ttc atc tgc acc acc ggc aag ctg ccc gtg	48
	Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val	
	1 5 10 15	
	ccc tgg ccc acc ctc gtg acc acc ttc ggc tac ggc ctg cag tgc ttc	96
	Pro Trp Pro Thr Leu Val Thr Thr Phe Gly Tyr Gly Leu Gln Cys Phe	
	20 25 30	
45	gcc cgc tac ccc gac cac atg aag cgg cac gac ttc ttc aag tcc gcc	144
	Ala Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser Ala	
	35 40 45	
50	atg ccc gaa ggc tac gtc cag gag cgc acc atc ttc ttc aag gac gac	192
	Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp	
	50 55 60	
55	ggc aac tac aag acc cgc gcc gag gtg aag ttc gag ggc gac acc ctg	240
	Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu	
	65 70 75 80	

	gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag gac ggc aac	288
	Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn	
	85 90 95	
5	atc ctg ggg cac aag ctg gag tac aac tac aac agc cac aac gtc tat	336
	Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr	
	100 105 110	
10	atc atg gcc gac aag cag aag aac ggc atc aag gtg aac ttc aag atc	384
	Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile	
	115 120 125	
15	cgc cac aac atc gag gac ggc agc gtg cag ctc gcc gac cac tac cag	432
	Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln	
	130 135 140	
20	cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc gac aac cac	480
	Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His	
	145 150 155 160	
	tac ctg agc cac cag tcc gcc ctg agc aaa gac ccc aac gag aag cgc	528
	Tyr Leu Ser His Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg	
	165 170 175	
25	gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg atc act ctc	576
	Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr Leu	
	180 185 190	
30	ggc atg gac gag ctg tac aag	597
	Gly Met Asp Glu Leu Tyr Lys	
	195	
35	YFP F2A, Y203H mutation + Met @ posit. 1	
	SEQ ID NOS:180 & 181	
40	atg ggc aag ctg acc ctg aag ttc atc tgc acc acc ggc aag ctg ccc	48
	Met Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro	
	1 5 10 15	
45	gtg ccc tgg ccc acc ctc gtg acc acc ttc ggc tac ggc ctg cag tgc	96
	Val Pro Trp Pro Thr Leu Val Thr Thr Phe Gly Tyr Gly Leu Gln Cys	
	20 25 30	
50	ttc gcc cgc tac ccc gac cac atg aag cgg cac gac ttc ttc aag tcc	144
	Phe Ala Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser	
	35 40 45	
	gcc atg ccc gaa ggc tac gtc cag gag cgc acc atc ttc ttc aag gac	192
	Ala Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp	
	50 55 60	
55	gac ggc aac tac aag acc cgc gcc gag gtg aag ttc gag ggc gac acc	240
	Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr	
	65 70 75 80	

	ctg gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag gac ggc	288
	Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly	
	85 90 95	
5	aac atc ctg ggg cac aag ctg gag tac aac tac aac agc cac aac gtc	336
	Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val	
	100 105 110	
10	tat atc atg gcc gac aag cag aag aac ggc atc aag gtg aac ttc aag	384
	Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys	
	115 120 125	
15	atc cgc cac aac atc gag gac ggc agc gtg cag ctc gcc gac cac tac	432
	Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr	
	130 135 140	
20	cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc gac aac	480
	Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn	
	145 150 155 160	
25	cac tac ctg agc cac cag tcc gcc ctg agc aaa gac ccc aac gag aag	528
	His Tyr Leu Ser His Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys	
	165 170 175	
30	cgc gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg atc act	576
	Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr	
	180 185 190	
35	ctc ggc atg gac gag ctg tac aag	600
	Leu Gly Met Asp Glu Leu Tyr Lys	
	195 200	
35	SEYFP F2A frag (aa 40-239 of SEYFP) + Met @ pos. 1	
	SEQ ID NOS:182 & 183	
40	atg ggc aag ctg acc ctg aag ttc atc tgc acc acc ggc aag ctg ccc	48
	Met Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro	
	1 5 10 15	
45	gtg ccc tgg ccc acc ctc gtg acc acc ctg ggc tac ggc ctg cag tgc	96
	Val Pro Trp Pro Thr Leu Val Thr Thr Leu Gly Tyr Gly Leu Gln Cys	
	20 25 30	
50	ttc gcc cgc tac ccc gac cac atg aag cgg cac gac ttc ttc aag tcc	144
	Phe Ala Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser	
	35 40 45	
55	gcc atg ccc gaa ggc tac gtc cag gag cgc acc atc ttc ttc aag gac	192
	Ala Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp	
	50 55 60	
55	gac ggc aac tac aag acc cgc gcc gag gtg aag ttc gag ggc gac acc	240
	Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr	
	65 70 75 80	

	ctg gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag gac ggc	288
	Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly	
	85 90 95	
5	aac atc ctg ggg cac aag ctg gag tac aac tac aac agc cac aac gtc	336
	Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val	
	100 105 110	
10	tat atc acc gcc gac aag cag aag aac ggc atc aag gcc aac ttc aag	384
	Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly Ile Lys Ala Asn Phe Lys	
	115 120 125	
15	atc cgc cac aac atc gag gac ggc ggc gtg cag ctc gcc gac cac tac	432
	Ile Arg His Asn Ile Glu Asp Gly Gly Val Gln Leu Ala Asp His Tyr	
	130 135 140	
20	cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc gac aac	480
	Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn	
	145 150 155 160	
	cac tac ctg agc tac cag tcc gcc ctg agc aaa gac ccc aac gag aag	528
	His Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys	
	165 170 175	
25	cgc gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg atc act	576
	Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr	
	180 185 190	
30	ctc ggc atg gac gag ctg tac aag	600
	Leu Gly Met Asp Glu Leu Tyr Lys	
	195 200	
35	VenusF2A, S175G mutation	
	SEQ ID NOS:184 & 185	
40	ggc aag ctg acc ctg aag ttc atc tgc acc acc ggc aag ctg ccc gtg	48
	Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val	
	1 5 10 15	
	ccc tgg ccc acc ctc gtg acc acc ttc ggc tac ggc ctg cag tgc ttc	96
	Pro Trp Pro Thr Leu Val Thr Thr Phe Gly Tyr Gly Leu Gln Cys Phe	
	20 25 30	
45	gcc cgc tac ccc gac cac atg aag cgg cac gac ttc ttc aag tcc gcc	144
	Ala Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser Ala	
	35 40 45	
50	atg ccc gaa ggc tac gtc cag gag cgc acc atc ttc ttc aag gac gac	192
	Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp	
	50 55 60	
55	ggc aac tac aag acc cgc gcc gag gtg aag ttc gag ggc gac acc ctg	240
	Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu	
	65 70 75 80	

	gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag gac ggc aac	288
	Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn	
	85 90 95	
5	atc ctg ggg cac aag ctg gag tac aac tac aac agc cac aac gtc tat	336
	Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr	
	100 105 110	
10	atc atg gcc gac aag cag aag aac ggc atc aag gtg aac ttc aag atc	384
	Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile	
	115 120 125	
15	cgc cac aac atc gag gac ggc ggc gtg cag ctc gcc gac cac tac cag	432
	Arg His Asn Ile Glu Asp Gly Gly Val Gln Leu Ala Asp His Tyr Gln	
	130 135 140	
20	cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc gac aac cac	480
	Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His	
	145 150 155 160	
	tac ctg agc tac cag tcc gcc ctg agc aaa gac ccc aac gag aag cgc	528
	Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg	
	165 170 175	
25	gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg atc act ctc	576
	Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr Leu	
	180 185 190	
30	ggc atg gac gag ctg tac aag	597
	Gly Met Asp Glu Leu Tyr Lys	
	195	
35	VenusF2A, S175G mutation + Met @ posit. 1	
	SEQ ID NOS:186 & 187	
40	atg ggc aag ctg acc ctg aag ttc atc tgc acc acc ggc aag ctg ccc	48
	Met Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro	
	1 5 10 15	
	gtg ccc tgg ccc acc ctc gtg acc acc ttc ggc tac ggc ctg cag tgc	96
	Val Pro Trp Pro Thr Leu Val Thr Thr Phe Gly Tyr Gly Leu Gln Cys	
	20 25 30	
45	ttc gcc cgc tac ccc gac cac atg aag cgg cac gac ttc ttc aag tcc	144
	Phe Ala Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser	
	35 40 45	
50	gcc atg ccc gaa ggc tac gtc cag gag cgc acc atc ttc ttc aag gac	192
	Ala Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp	
	50 55 60	
55	gac ggc aac tac aag acc cgc gcc gag gtg aag ttc gag ggc gac acc	240
	Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr	
	65 70 75 80	



	ctg gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag gac ggc	288
	Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly	
	85 90 95	
5	aac atc ctg ggg cac aag ctg gag tac aac tac aac agc cac aac gtc	336
	Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val	
	100 105 110	
10	tat atc atg gcc gac aag cag aag aac ggc atc aag gtg aac ttc aag	384
	Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys	
	115 120 125	
15	atc cgc cac aac atc gag gac ggc ggc gtg cag ctc gcc gac cac tac	432
	Ile Arg His Asn Ile Glu Asp Gly Gly Val Gln Leu Ala Asp His Tyr	
	130 135 140	
20	cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc gac aac	480
	Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn	
	145 150 155 160	
	cac tac ctg agc tac cag tcc gcc ctg agc aaa gac ccc aac gag aag	528
	His Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys	
	165 170 175	
25	cgc gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg atc act	576
	Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr	
	180 185 190	
30	ctc ggc atg gac gag ctg tac aag	600
	Leu Gly Met Asp Glu Leu Tyr Lys	
	195 200	
35	VenusF2A, M153T, S175G mutations	
	SEQ ID NOS:188 & 189	
40	ggc aag ctg acc ctg aag ttc atc tgc acc acc ggc aag ctg ccc gtg	48
	Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val	
	1 5 10 15	
45	ccc tgg ccc acc ctc gtg acc acc ttc ggc tac ggc ctg cag tgc ttc	96
	Pro Trp Pro Thr Leu Val Thr Thr Phe Gly Tyr Gly Leu Gln Cys Phe	
	20 25 30	
	gcc cgc tac ccc gac cac atg aag cgg cac gac ttc ttc aag tcc gcc	144
	Ala Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser Ala	
	35 40 45	
50	atg ccc gaa ggc tac gtc cag gag cgc acc atc ttc ttc aag gac gac	192
	Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp	
	50 55 60	
55	ggc aac tac aag acc cgc gcc gag gtg aag ttc gag ggc gac acc ctg	240
	Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu	
	65 70 75 80	

	gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag gac ggc aac	288
	Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn	
	85 90 95	
5	atc ctg ggg cac aag ctg gag tac aac tac aac agc cac aac gtc tat	336
	Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr	
	100 105 110	
10	atc acc gcc gac aag cag aag aac ggc atc aag gtg aac ttc aag atc	384
	Ile Thr Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile	
	115 120 125	
15	cgc cac aac atc gag gac ggc ggc gtg cag ctc gcc gac cac tac cag	432
	Arg His Asn Ile Glu Asp Gly Gly Val Gln Leu Ala Asp His Tyr Gln	
	130 135 140	
20	cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc gac aac cac	480
	Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His	
	145 150 155 160	
	tac ctg agc tac cag tcc gcc ctg agc aaa gac ccc aac gag aag cgc	528
	Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg	
	165 170 175	
25	gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg atc act ctc	576
	Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr Leu	
	180 185 190	
30	ggc atg gac gag ctg tac aag	597
	Gly Met Asp Glu Leu Tyr Lys	
	195	
35	VenusF2A, M153T, S175G mutations + Met @ posit. 1	
	SEQ ID NOS:190 & 191	
40	atg ggc aag ctg acc ctg aag ttc atc tgc acc acc ggc aag ctg ccc	48
	Met Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro	
	1 5 10 15	
	gtg ccc tgg ccc acc ctc gtg acc acc ttc ggc tac ggc ctg cag tgc	96
	Val Pro Trp Pro Thr Leu Val Thr Thr Phe Gly Tyr Gly Leu Gln Cys	
	20 25 30	
45	ttc gcc cgc tac ccc gac cac atg aag cgg cac gac ttc ttc aag tcc	144
	Phe Ala Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser	
	35 40 45	
50	gcc atg ccc gaa ggc tac gtc cag gag cgc acc atc ttc ttc aag gac	192
	Ala Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp	
	50 55 60	
55	gac ggc aac tac aag acc cgc gcc gag gtg aag ttc gag ggc gac acc	240
	Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr	
	65 70 75 80	

	ctg gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag gac ggc	288
	Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly	
	85 90 95	
5	aac atc ctg ggg cac aag ctg gag tac aac tac aac agc cac aac gtc	336
	Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val	
	100 105 110	
10	tat atc acc gcc gac aag cag aag aac ggc atc aag gtg aac ttc aag	384
	Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys	
	115 120 125	
15	atc cgc cac aac atc gag gac ggc ggc gtg cag ctc gcc gac cac tac	432
	Ile Arg His Asn Ile Glu Asp Gly Gly Val Gln Leu Ala Asp His Tyr	
	130 135 140	
20	cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc gac aac	480
	Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn	
	145 150 155 160	
	cac tac ctg agc tac cag tcc gcc ctg agc aaa gac ccc aac gag aag	528
	His Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys	
	165 170 175	
25	cgc gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg atc act	576
	Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr	
	180 185 190	
30	ctc ggc atg gac gag ctg tac aag	600
	Leu Gly Met Asp Glu Leu Tyr Lys	
	195 200	
35	VenusF2A, V163A, S175G mutations	
	SEQ ID NOS:192 & 193	
40	ggc aag ctg acc ctg aag ttc atc tgc acc acc ggc aag ctg ccc gtg	48
	Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val	
	1 5 10 15	
	ccc tgg ccc acc ctc gtg acc acc ttc ggc tac ggc ctg cag tgc ttc	96
	Pro Trp Pro Thr Leu Val Thr Thr Phe Gly Tyr Gly Leu Gln Cys Phe	
	20 25 30	
45	gcc cgc tac ccc gac cac atg aag cgg cac gac ttc ttc aag tcc gcc	144
	Ala Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser Ala	
	35 40 45	
50	atg ccc gaa ggc tac gtc cag gag cgc acc atc ttc ttc aag gac gac	192
	Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp	
	50 55 60	
55	ggc aac tac aag acc cgc gcc gag gtg aag ttc gag ggc gac acc ctg	240
	Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu	
	65 70 75 80	

	gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag gac ggc aac	288
	Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn	
	85 90 95	
5	atc ctg ggg cac aag ctg gag tac aac tac aac agc cac aac gtc tat	336
	Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr	
	100 105 110	
10	atc atg gcc gac aag cag aag aac ggc atc aag gcc aac ttc aag atc	384
	Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Ala Asn Phe Lys Ile	
	115 120 125	
15	cgc cac aac atc gag gac ggc ggc gtg cag ctc gcc gac cac tac cag	432
	Arg His Asn Ile Glu Asp Gly Gly Val Gln Leu Ala Asp His Tyr Gln	
	130 135 140	
20	cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc gac aac cac	480
	Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His	
	145 150 155 160	
	tac ctg agc tac cag tcc gcc ctg agc aaa gac ccc aac gag aag cgc	528
	Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg	
	165 170 175	
25	gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg atc act ctc	576
	Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr Leu	
	180 185 190	
30	ggc atg gac gag ctg tac aag	597
	Gly Met Asp Glu Leu Tyr Lys	
	195	
35	VenusF2A, V163A, S175G mutations + Met @ pos. 1	
	SEQ ID NOS:194 & 195	
40	atg ggc aag ctg acc ctg aag ttc atc tgc acc acc ggc aag ctg ccc	48
	Met Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro	
	1 5 10 15	
45	gtg ccc tgg ccc acc ctc gtg acc acc ttc ggc tac ggc ctg cag tgc	96
	Val Pro Trp Pro Thr Leu Val Thr Thr Phe Gly Tyr Gly Leu Gln Cys	
	20 25 30	
	ttc gcc cgc tac ccc gac cac atg aag cgg cac gac ttc ttc aag tcc	144
	Phe Ala Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser	
	35 40 45	
50	gcc atg ccc gaa ggc tac gtc cag gag cgc acc atc ttc ttc aag gac	192
	Ala Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp	
	50 55 60	
55	gac ggc aac tac aag acc cgc gcc gag gtg aag ttc gag ggc gac acc	240
	Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr	
	65 70 75 80	

	ctg gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag gac ggc	288
	Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly	
	85 90 95	
5	aac atc ctg ggg cac aag ctg gag tac aac tac aac agc cac aac gtc	336
	Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val	
	100 105 110	
10	tat atc atg gcc gac aag cag aag aac ggc atc aag gcc aac ttc aag	384
	Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Ala Asn Phe Lys	
	115 120 125	
15	atc cgc cac aac atc gag gac ggc ggc gtg cag ctc gcc gac cac tac	432
	Ile Arg His Asn Ile Glu Asp Gly Gly Val Gln Leu Ala Asp His Tyr	
	130 135 140	
20	cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc gac aac	480
	Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn	
	145 150 155 160	
	cac tac ctg agc tac cag tcc gcc ctg agc aaa gac ccc aac gag aag	528
	His Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys	
	165 170 175	
25	cgc gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg atc act	576
	Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr	
	180 185 190	
30	ctc ggc atg gac gag ctg tac aag	600
	Leu Gly Met Asp Glu Leu Tyr Lys	
	195 200	
35	VenusF2A, F46L/F64L/M153T/V163A/S175G mutations	
	SEQ ID NOS:196 & 197	
40	ggc aag ctg acc ctg aag ctg atc tgc acc acc ggc aag ctg ccc gtg	48
	Gly Lys Leu Thr Leu Lys Leu Ile Cys Thr Thr Gly Lys Leu Pro Val	
	1 5 10 15	
45	ccc tgg ccc acc ctc gtg acc acc ctc ggc tac ggc ctg cag tgc ttc	96
	Pro Trp Pro Thr Leu Val Thr Thr Leu Gly Tyr Gly Leu Gln Cys Phe	
	20 25 30	
50	gcc cgc tac ccc gac cac atg aag cgg cac gac ttc ttc aag tcc gcc	144
	Ala Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser Ala	
	35 40 45	
	atg ccc gaa ggc tac gtc cag gag cgc acc atc ttc ttc aag gac gac	192
	Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp	
	50 55 60	
55	ggc aac tac aag acc cgc gcc gag gtg aag ttc gag ggc gac acc ctg	240
	Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu	
	65 70 75 80	

	gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag gac ggc aac	288
	Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn	
	85 90 95	
5	atc ctg ggg cac aag ctg gag tac aac tac aac agc cac aac gtc tat	336
	Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr	
	100 105 110	
10	atc acc gcc gac aag cag aag aac ggc atc aag gcc aac ttc aag atc	384
	Ile Thr Ala Asp Lys Gln Lys Asn Gly Ile Lys Ala Asn Phe Lys Ile	
	115 120 125	
15	cgc cac aac atc gag gac ggc ggc gtg cag ctc gcc gac cac tac cag	432
	Arg His Asn Ile Glu Asp Gly Gly Val Gln Leu Ala Asp His Tyr Gln	
	130 135 140	
20	cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc gac aac cac	480
	Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His	
	145 150 155 160	
25	tac ctg agc tac cag tcc gcc ctg agc aaa gac ccc aac gag aag cgc	528
	Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg	
	165 170 175	
30	gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg atc act ctc	576
	Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr Leu	
	180 185 190	
35	ggc atg gac gag ctg tac aag	597
	Gly Met Asp Glu Leu Tyr Lys	
	195	
35	Venus F2A F46L/F64L/M153T/V163A/S175G mutations + Met @ pos. 1	
	SEQ ID NOS:198 & 199	
40	atg ggc aag ctg acc ctg aag ctg atc tgc acc acc ggc aag ctg ccc	48
	Met Gly Lys Leu Thr Leu Lys Leu Ile Cys Thr Thr Gly Lys Leu Pro	
	1 5 10 15	
45	gtg ccc tgg ccc acc ctc gtg acc acc ctc ggc tac ggc ctg cag tgc	96
	Val Pro Trp Pro Thr Leu Val Thr Thr Leu Gly Tyr Gly Leu Gln Cys	
	20 25 30	
50	ttc gcc cgc tac ccc gac cac atg aag cgg cac gac ttc ttc aag tcc	144
	Phe Ala Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser	
	35 40 45	
55	gcc atg ccc gaa ggc tac gtc cag gag cgc acc atc ttc ttc aag gac	192
	Ala Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp	
	50 55 60	
55	gac ggc aac tac aag acc cgc gcc gag gtg aag ttc gag ggc gac acc	240
	Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr	
	65 70 75 80	

	ctg gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag gac ggc	288
	Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly	
	85 90 95	
5	aac atc ctg ggg cac aag ctg gag tac aac tac aac agc cac aac gtc	336
	Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val	
	100 105 110	
10	tat atc acc gcc gac aag cag aag aac ggc atc aag gcc aac ttc aag	384
	Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly Ile Lys Ala Asn Phe Lys	
	115 120 125	
15	atc cgc cac aac atc gag gac ggc ggc gtg cag ctc gcc gac cac tac	432
	Ile Arg His Asn Ile Glu Asp Gly Gly Val Gln Leu Ala Asp His Tyr	
	130 135 140	
20	cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc gac aac	480
	Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn	
	145 150 155 160	
	cac tac ctg agc tac cag tcc gcc ctg agc aaa gac ccc aac gag aag	528
	His Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys	
	165 170 175	
25	cgc gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg atc act	576
	Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr	
	180 185 190	
30	ctc ggc atg gac gag ctg tac aag	600
	Leu Gly Met Asp Glu Leu Tyr Lys	
	195 200	
35	YFP F1B (aa residues 1-103 of YFP) pos. 1 Met removed	
	SEQ ID NOS:200 & 201	
40	gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc	48
	Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val	
	1 5 10 15	
45	gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag	96
	Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu	
	20 25 30	
	ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc tgc	144
	Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys	
	35 40 45	
50	acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ttc	192
	Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe	
	50 55 60	
55	ggc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag cgg	240
	Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg	
	65 70 75 80	

	cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc	288
	His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg	
	85 90 95	
5	acc atc ttc ttc aag gac	306
	Thr Ile Phe Phe Lys Asp	
	100	
10	EGFP F1B, 65L/66T/69V/73S	
	SEQ ID NOS:202 & 203	
15	atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg	48
	Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu	
	1 5 10 15	
20	gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc	96
	Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly	
	20 25 30	
25	gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc	144
	Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile	
	35 40 45	
30	tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc	192
	Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr	
	50 55 60	
35	ctc acc tac ggc gtg cag tgc ttc agc cgc tac ccc gac cac atg aag	240
	Leu Thr Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys	
	65 70 75 80	
40	cgg cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag	288
	Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu	
	85 90 95	
45	cgc acc atc ttc ttc aag gac	309
	Arg Thr Ile Phe Phe Lys Asp	
	100	
50	EGFP F1B, 65L/66T/69V/73S pos.1 Met removed	
	SEQ ID NOS:204 & 205	
55	gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc	48
	Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val	
	1 5 10 15	
60	gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag	96
	Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu	
	20 25 30	
65	ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc tgc	144
	Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys	
	35 40 45	



	acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ctc	192
	Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Leu	
	50 55 60	
5	acc tac ggc gtg cag tgc ttc agc cgc tac ccc gac cac atg aag cgg	240
	Thr Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys Arg	
	65 70 75 80	
10	cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc	288
	His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg	
	85 90 95	
15	acc atc ttc ttc aag gac	306
	Thr Ile Phe Phe Lys Asp	
	100	
20	YFP F1B K79R mutation	
	SEQ ID NOS:206 & 207	
	atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg	48
	Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu	
	1 5 10 15	
25	gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc	96
	Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly	
	20 25 30	
30	gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc	144
	Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile	
	35 40 45	
35	tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc	192
	Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr	
	50 55 60	
40	ttc ggc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg cgc	240
	Phe Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Arg	
	65 70 75 80	
45	cgg cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag	288
	Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu	
	85 90 95	
50	cgc acc atc ttc ttc aag gac	309
	Arg Thr Ile Phe Phe Lys Asp	
	100	
50	YFP F1B K79R mutation and pos. 1 Met removed	
	SEQ ID NOS:208 & 209	
55	gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc	48
	Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val	
	1 5 10 15	

	gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag	96
	Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu	
	20 25 30	
5	ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc tgc	144
	Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys	
	35 40 45	
10	acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ttc	192
	Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe	
	50 55 60	
15	ggc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg cgc cgg	240
	Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Arg Arg	
	65 70 75 80	
20	cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc	288
	His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg	
	85 90 95	
	acc atc ttc ttc aag gac	306
	Thr Ile Phe Phe Lys Asp	
	100	
25	YFP F1B Y66F mutation	
	SEQ ID NOS:210 & 211	
30	atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg	48
	Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu	
	1 5 10 15	
35	gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc	96
	Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly	
	20 25 30	
40	gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc	144
	Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile	
	35 40 45	
45	tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc	192
	Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr	
	50 55 60	
50	ttc ggc ttc ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag	240
	Phe Gly Phe Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys	
	65 70 75 80	
55	cgg cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag	288
	Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu	
	85 90 95	
	cgc acc atc ttc ttc aag gac	309
	Arg Thr Ile Phe Phe Lys Asp	
	100	

YFP F1B Y66F mutation and pos. 1 Met removed  
SEQ ID NOS:212 & 213

5	gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc Val Ser Lys Gly Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val 1 5 10 15	48
10	gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu 20 25 30	96
15	ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc tgc Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys 35 40 45	144
	acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ttc Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe 50 55 60	192
20	ggc ttc ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag cgg Gly Phe Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg 65 70 75 80	240
25	cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg 85 90 95	288
30	acc atc ttc ttc aag gac Thr Ile Phe Phe Lys Asp 100	306

35 YFP F1B Q69K mutation  
SEQ ID NOS:214 & 215

40	atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu 1 5 10 15	48
45	gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly 20 25 30	96
	gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile 35 40 45	144
50	tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr 50 55 60	192
55	ttc ggc tac ggc ctg aag tgc ttc gcc cgc tac ccc gac cac atg aag Phe Gly Tyr Gly Leu Lys Cys Phe Ala Arg Tyr Pro Asp His Met Lys 65 70 75 80	240

	cgg cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu 85 90 95	288
5	cgc acc atc ttc ttc aag gac Arg Thr Ile Phe Phe Lys Asp 100	309
10	YFP F1B Q69K mutation and pos.1 Metremoved SEQ ID NOS:216 & 217	
	gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val 1 5 10 15	48
15		
	gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu 20 25 30	96
20		
	ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc tgc Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys 35 40 45	144
25		
	acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ttc Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe 50 55 60	192
30		
	ggc tac ggc ctg aag tgc ttc gcc cgc tac ccc gac cac atg aag cgg Gly Tyr Gly Leu Lys Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg 65 70 75 80	240
35		
	cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg 85 90 95	288
40		
	acc atc ttc ttc aag gac Thr Ile Phe Phe Lys Asp 100	306
	YFP F1B K79R mutation SEQ ID NOS:218 & 219	
45		
	atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu 1 5 10 15	48
50		
	gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly 20 25 30	96
55		
	gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile 35 40 45	144

	tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc	192
	Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr	
	50 55 60	
5	ttc ggc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg cgc	240
	Phe Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Arg	
	65 70 75 80	
10	cgg cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag	288
	Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu	
	85 90 95	
15	cgc acc atc ttc ttc aag gac	309
	Arg Thr Ile Phe Phe Lys Asp	
	100	
20	YFP F1B K79R mutation and pos. 1 Met removed	
	SEQ ID NOS:220 & 221	
	gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc	48
	Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val	
	1 5 10 15	
25	gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag	96
	Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu	
	20 25 30	
30	ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc tgc	144
	Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys	
	35 40 45	
35	acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ttc	192
	Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe	
	50 55 60	
40	ggc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg cgc cgg	240
	Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Arg Arg	
	65 70 75 80	
45	cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc	288
	His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg	
	85 90 95	
50	acc atc ttc ttc aag gac	306
	Thr Ile Phe Phe Lys Asp	
	100	
50	citrine F1B, V68L, Q69M mutations	
	SEQ ID NOS:222 & 223	
55	atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg	48
	Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu	
	1 5 10 15	

	gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc	96
	Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly	
	20 25 30	
5	gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc	144
	Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile	
	35 40 45	
10	tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc	192
	Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr	
	50 55 60	
15	ttc ggc tac ggc ctg atg tgc ttc gcc cgc tac ccc gac cac atg aag	240
	Phe Gly Tyr Gly Leu Met Cys Phe Ala Arg Tyr Pro Asp His Met Lys	
	65 70 75 80	
20	cgg cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag	288
	Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu	
	85 90 95	
25	cgc acc atc ttc ttc aag gac	309
	Arg Thr Ile Phe Phe Lys Asp	
	100	
30	citrine F1B, V68L, Q69M mutations and pos.1 Met removed	
	SEQ ID NOS:224 & 225	
30	gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc	48
	Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val	
	1 5 10 15	
35	gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag	96
	Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu	
	20 25 30	
40	ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc tgc	144
	Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys	
	35 40 45	
45	acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ttc	192
	Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe	
	50 55 60	
50	ggc tac ggc ctg atg tgc ttc gcc cgc tac ccc gac cac atg aag cgg	240
	Gly Tyr Gly Leu Met Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg	
	65 70 75 80	
55	cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc	288
	His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg	
	85 90 95	
55	acc atc ttc ttc aag gac	306
	Thr Ile Phe Phe Lys Asp	
	100	

Venus F1B F46L, F64L mutations  
SEQ ID NOS:226 & 227

5	atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu 1 5 10 15	48
10	gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly 20 25 30	96
15	gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ctg atc Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Leu Ile 35 40 45	144
20	tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr 50 55 60	192
25	ctg ggc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag Leu Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys 65 70 75 80	240
30	cgg cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu 85 90 95	288
35	cgc acc atc ttc ttc aag gac Arg Thr Ile Phe Phe Lys Asp 100	309

35 Venus F1B F46L, F64L mutations and pos.1 Met removed  
SEQ ID NOS:228 & 229

40	gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val 1 5 10 15	48
45	gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu 20 25 30	96
50	ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ctg atc tgc Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Leu Ile Cys 35 40 45	144
55	acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ctg Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Leu 50 55 60	192
60	ggc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag cgg Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg 65 70 75 80	240

	cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc	288
	His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg	
	85 90 95	
5	acc atc ttc ttc aag gac	306
	Thr Ile Phe Phe Lys Asp	
	100	
10	YFP F1B F46L mutation	
	SEQ ID NOS:230 & 231	
15	atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg	48
	Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu	
	1 5 10 15	
20	gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc	96
	Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly	
	20 25 30	
25	gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ctg atc	144
	Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Leu Ile	
	35 40 45	
30	tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc	192
	Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr	
	50 55 60	
35	ttc ggc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag	240
	Phe Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys	
	65 70 75 80	
40	cgg cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag	288
	Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu	
	85 90 95	
45	cgc acc atc ttc ttc aag gac	309
	Arg Thr Ile Phe Phe Lys Asp	
	100	
50	YFP F1B F46L mutation and posit. 1 Met removed	
	SEQ ID NOS:232 & 233	
55	gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc	48
	Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val	
	1 5 10 15	
60	gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag	96
	Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu	
	20 25 30	
65	ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ctg atc tgc	144
	Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Leu Ile Cys	
	35 40 45	



	acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ttc	192
	Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe	
	50 55 60	
5	ggc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag cgg	240
	Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg	
	65 70 75 80	
10	cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc	288
	His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg	
	85 90 95	
15	acc atc ttc ttc aag gac	306
	Thr Ile Phe Phe Lys Asp	
	100	
20	CFP F1B F64L mutation	
	SEQ ID NOS:234 & 235	
25	atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg	48
	Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu	
	1 5 10 15	
30	gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc	96
	Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly	
	20 25 30	
35	gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc	144
	Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile	
	35 40 45	
40	tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc	192
	Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr	
	50 55 60	
45	ctg ggc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag	240
	Leu Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys	
	65 70 75 80	
50	cgg cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag	288
	Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu	
	85 90 95	
55	cgc acc atc ttc ttc aag gac	309
	Arg Thr Ile Phe Phe Lys Asp	
	100	
50	CFP F1B F64L mutation and pos. 1 Met removed	
	SEQ ID NOS:236 & 237	
55	gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc	48
	Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val	
	1 5 10 15	

	gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag	96
	Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu	
	20 25 30	
5	ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc tgc	144
	Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys	
	35 40 45	
10	acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ctg	192
	Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Leu	
	50 55 60	
15	ggc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag cgg	240
	Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg	
	65 70 75 80	
20	cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc	288
	His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg	
	85 90 95	
25	acc atc ttc ttc aag gac	306
	Thr Ile Phe Phe Lys Asp	
	100	
30	CFP F1B Y66W mutation	
	SEQ ID NOS:238 & 239	
35	atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg	48
	Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu	
	1 5 10 15	
40	gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc	96
	Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly	
	20 25 30	
45	gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc	144
	Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile	
	35 40 45	
50	tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc	192
	Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr	
	50 55 60	
55	ttc ggc tgg ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag	240
	Phe Gly Trp Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys	
	65 70 75 80	
60	cgg cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag	288
	Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu	
	85 90 95	
65	cgc acc atc ttc ttc aag gac	309
	Arg Thr Ile Phe Phe Lys Asp	
	100	

CFP F1B Y66W mutation and pos.1 Met removed  
SEQ ID NOS:240 & 241

5	gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val 1 5 10 15	48
10	gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu 20 25 30	96
15	ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc tgc Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys 35 40 45	144
	acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ttc Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe 50 55 60	192
20	ggc tgg ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag cgg Gly Trp Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg 65 70 75 80	240
25	cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg 85 90 95	288
30	acc atc ttc ttc aag gac Thr Ile Phe Phe Lys Asp 100	306

35 CFP F1B S65A mutation  
SEQ ID NOS:242 & 243

40	atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu 1 5 10 15	48
45	gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly 20 25 30	96
	gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile 35 40 45	144
50	tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr 50 55 60	192
55	ttc gcc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag Phe Ala Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys 65 70 75 80	240

	cgg cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu 85                    90                    95	288
5	cgc acc atc ttc ttc aag gac Arg Thr Ile Phe Phe Lys Asp 100	309
10	CFP F1B S65A mutation and pos. 1 Met removed SEQ ID NOS:244 & 245	
15	gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val 1                    5                    10                    15	48
20	gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu 20                    25                    30	96
25	ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc tgc Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys 35                    40                    45	144
	acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ttc Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe 50                    55                    60	192
30	gcc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag cgg Ala Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg 65                    70                    75                    80	240
35	cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg 85                    90                    95	288
40	acc atc ttc ttc aag gac Thr Ile Phe Phe Lys Asp 100	306
45	CFP F1B, S65A, Y66W, and S72A mutations SEQ ID NOS:246 & 247	
	atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu 1                    5                    10                    15	48
50	gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly 20                    25                    30	96
55	gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile 35                    40                    45	144

	tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc	192
	Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr	
	50 55 60	
5	ttc gcc tgg ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag	240
	Phe Ala Trp Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys	
	65 70 75 80	
10	cgg cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag	288
	Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu	
	85 90 95	
15	cgc acc atc ttc ttc aag gac	309
	Arg Thr Ile Phe Phe Lys Asp	
	100	
20	CFP F1B, S65A, Y66W, and S72A mutations, and posit. 1 Met removed SEQ ID NOS:248 & 249	
25	gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc	48
	Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val	
	1 5 10 15	
30	gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag	96
	Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu	
	20 25 30	
35	ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc tgc	144
	Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys	
	35 40 45	
40	acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ttc	192
	Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe	
	50 55 60	
45	gcc tgg ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag cgg	240
	Ala Trp Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg	
	65 70 75 80	
50	cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc	288
	His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg	
	85 90 95	
55	acc atc ttc ttc aag gac	306
	Thr Ile Phe Phe Lys Asp	
	100	
55	CFP F1B, F64L, S65T, and Y66W mutations SEQ ID NOS:250 & 251	
55	atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg	48
	Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu	
	1 5 10 15	

	gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc	96										
	Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly											
	20 25 30											
5	gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc	144										
	Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile											
	35 40 45											
10	tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc	192										
	Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr											
	50 55 60											
15	ctc acc tgg ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag	240										
	Leu Thr Trp Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys											
	65 70 75 80											
20	cgg cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag	288										
	Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu											
	85 90 95											
25	cgc acc atc ttc ttc aag gac	309										
	Arg Thr Ile Phe Phe Lys Asp											
	100											
30	CFP F1B, F64L ,S65T, and Y66W mutations, and pos. 1 Met removed SEQ ID NOS:252 & 253											
	gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc	48										
	Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val											
	1 5 10 15											
35	gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag	96										
	Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu											
	20 25 30											
40	ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc tgc	144										
	Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys											
	35 40 45											
45	acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ctc	192										
	Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Leu											
	50 55 60											
50	acc tgg ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag cgg	240										
	Thr Trp Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg											
	65 70 75 80											
55	cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc	288										
	His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg											
	85 90 95											
	acc atc ttc ttc aag gac	306										
	Thr Ile Phe Phe Lys Asp											
	100											

BFP F1B, Y66H mutation  
SEQ ID NOS:254 & 255

5	atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg	48
	Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu	
	1 5 10 15	
10	gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc	96
	Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly	
	20 25 30	
15	gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc	144
	Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile	
	35 40 45	
	tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc	192
	Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr	
	50 55 60	
20	ttc ggc cac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag	240
	Phe Gly His Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys	
	65 70 75 80	
25	cgg cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag	288
	Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu	
	85 90 95	
30	cgc acc atc ttc ttc aag gac	309
	Arg Thr Ile Phe Phe Lys Asp	
	100	

35 BFP F1B, Y66H mutation and pos.1 Met removed  
SEQ ID NOS:256 & 257

40	gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc	48
	Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val	
	1 5 10 15	
45	gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag	96
	Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu	
	20 25 30	
	ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc tgc	144
	Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys	
	35 40 45	
50	acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ttc	192
	Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe	
	50 55 60	
55	ggc cac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag cgg	240
	Gly His Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg	
	65 70 75 80	

	cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc	288
	His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg	
	85 90 95	
5	acc atc ttc ttc aag gac	306
	Thr Ile Phe Phe Lys Asp	
	100	
10	BFP F1B, F64L, Y66H mutations SEQ ID NOS:258 & 259	
	atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg	48
	Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu	
15	1 5 10 15	
	gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc	96
	Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly	
	20 25 30	
20		
	gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc	144
	Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile	
	35 40 45	
25		
	tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc	192
	Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr	
	50 55 60	
30		
	ctg ggc cac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag	240
	Leu Gly His Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys	
	65 70 75 80	
	cgg cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag	288
	Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu	
35	85 90 95	
	cgc acc atc ttc ttc aag gac	309
	Arg Thr Ile Phe Phe Lys Asp	
	100	
40		
	BFP F1B, F64L, Y66H mutations and pos.1 Met removed SEQ ID NOS:260 & 261	
45		
	gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc	48
	Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val	
	1 5 10 15	
50		
	gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag	96
	Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu	
	20 25 30	
55		
	ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc tgc	144
	Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys	
	35 40 45	



	acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ctg	192
	Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Leu	
	50 55 60	
5	ggc cac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag cgg	240
	Gly His Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg	
	65 70 75 80	
10	cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc	288
	His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg	
	85 90 95	
	acc atc ttc ttc aag gac	306
	Thr Ile Phe Phe Lys Asp	
15	100	
YFP F2B (aa residues 104-240 of EYFP) Met added @ pos. 1		
SEQ ID NOS:262 & 263		
20	atg gac ggc aac tac aag acc cgc gcc gag gtg aag ttc gag ggc gac	48
	Met Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp	
	1 5 10 15	
25	acc ctg gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag gac	96
	Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp	
	20 25 30	
30	ggc aac atc ctg ggg cac aag ctg gag tac aac tac aac agc cac aac	144
	Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn	
	35 40 45	
35	gtc tat atc atg gcc gac aag cag aag aac ggc atc aag gtg aac ttc	192
	Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe	
	50 55 60	
	aag atc cgc cac aac atc gag gac ggc agc gtg cag ctc gcc gac cac	240
	Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His	
	65 70 75 80	
40	tac cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc gac	288
	Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp	
	85 90 95	
45	aac cac tac ctg agc tac cag tcc gcc ctg agc aaa gac ccc aac gag	336
	Asn His Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu	
	100 105 110	
50	aag cgc gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg atc	384
	Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile	
	115 120 125	
55	act ctc ggc atg gac gag ctg tac aag	411
	Thr Leu Gly Met Asp Glu Leu Tyr Lys	
	130 135	

EGFP F2B(emerald), N146K, M153T, and I167T mutations  
SEQ ID NOS:264 & 265

[illegible]

EGFP F2B(emerald), N146K, M153T,I167T mutations and Met added @ pos. 1  
SEQ ID NOS:266 & 267

45	atg gac ggc aac tac aag acc cgc gcc gag gtg aag ttc gag ggc gac	48
	Met Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp	
	1 5 10 15	
50	acc ctg gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag gac	96
	Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp	
	20 25 30	
55	ggc aac atc ctg ggg cac aag ctg gag tac aac tac aac agc cac aag	144
	Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Lys	
	35 40 45	

	gtc tat atc acc gcc gac aag cag aag aac ggc atc aag gtg aac ttc	192
	Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe	
	50 55 60	
5	aag acc cgc cac aac atc gag gac ggc agc gtg cag ctc gcc gac cac	240
	Lys Thr Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His	
	65 70 75 80	
10	tac cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc gac	288
	Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp	
	85 90 95	
15	aac cac tac ctg agc acc cag tcc gcc ctg agc aaa gac ccc aac gag	336
	Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu	
	100 105 110	
20	aag cgc gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg atc	384
	Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile	
	115 120 125	
25	act ctc ggc atg gac gag ctg tac aag	411
	Thr Leu Gly Met Asp Glu Leu Tyr Lys	
	130 135	
30	YFP F2B Y203F mutation	
	SEQ ID NOS:268 & 269	
35	gac ggc aac tac aag acc cgc gcc gag gtg aag ttc gag ggc gac acc	48
	Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr	
	1 5 10 15	
40	ctg gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag gac ggc	96
	Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly	
	20 25 30	
45	aac atc ctg ggg cac aag ctg gag tac aac tac aac agc cac aac gtc	144
	Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val	
	35 40 45	
50	tat atc atg gcc gac aag cag aag aac ggc atc aag gtg aac ttc aag	192
	Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys	
	50 55 60	
55	atc cgc cac aac atc gag gac ggc agc gtg cag ctc gcc gac cac tac	240
	Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr	
	65 70 75 80	
60	cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc gac aac	288
	Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn	
	85 90 95	
65	cac tac ctg agc ttc cag tcc gcc ctg agc aaa gac ccc aac gag aag	336
	His Tyr Leu Ser Phe Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys	
	100 105 110	

	cgc gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg atc act	384
	Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr	
	115 120 125	
5	ctc ggc atg gac gag ctg tac aag	408
	Leu Gly Met Asp Glu Leu Tyr Lys	
	130 135	
10	YFP F2B Y203F mutation and Met added @ pos. 1	
	SEQ ID NOS:270 & 271	
15	atg gac ggc aac tac aag acc cgc gcc gag gtg aag ttc gag ggc gac	48
	Met Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp	
	1 5 10 15	
20	acc ctg gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag gac	96
	Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp	
	20 25 30	
25	ggc aac atc ctg ggg cac aag ctg gag tac aac tac aac agc cac aac	144
	Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn	
	35 40 45	
30	gtc tat atc atg gcc gac aag cag aag aac ggc atc aag gtg aac ttc	192
	Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe	
	50 55 60	
35	aag atc cgc cac aac atc gag gac ggc agc gtg cag ctc gcc gac cac	240
	Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His	
	65 70 75 80	
40	tac cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc gac	288
	Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp	
	85 90 95	
45	aac cac tac ctg agc ttc cag tcc gcc ctg agc aaa gac ccc aac gag	336
	Asn His Tyr Leu Ser Phe Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu	
	100 105 110	
50	aag cgc gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg atc	384
	Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile	
	115 120 125	
55	act ctc ggc atg gac gag ctg tac aag	411
	Thr Leu Gly Met Asp Glu Leu Tyr Lys	
	130 135	
50	YFP F2B Y203H mutation	
	SEQ ID NOS:272 & 273	
55	gac ggc aac tac aag acc cgc gcc gag gtg aag ttc gag ggc gac acc	48
	Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr	
	1 5 10 15	

	ctg gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag gac ggc	96
	Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly	
	20 25 30	
5	aac atc ctg ggg cac aag ctg gag tac aac tac aac agc cac aac gtc	144
	Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val	
	35 40 45	
10	tat atc atg gcc gac aag cag aag aac ggc atc aag gtg aac ttc aag	192
	Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys	
	50 55 60	
15	atc cgc cac aac atc gag gac ggc agc gtg cag ctc gcc gac cac tac	240
	Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr	
	65 70 75 80	
20	cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc gac aac	288
	Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn	
	85 90 95	
25	cac tac ctg agc cac cag tcc gcc ctg agc aaa gac ccc aac gag aag	336
	His Tyr Leu Ser His Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys	
	100 105 110	
30	cgc gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg atc act	384
	Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr	
	115 120 125	
35	ctc ggc atg gac gag ctg tac aag	408
	Leu Gly Met Asp Glu Leu Tyr Lys	
	130 135	
40	atg gac ggc aac tac aag acc cgc gcc gag gtg aag ttc gag ggc gac	48
	Met Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp	
	1 5 10 15	
45	acc ctg gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag gac	96
	Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp	
	20 25 30	
50	ggc aac atc ctg ggg cac aag ctg gag tac aac tac aac agc cac aac	144
	Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn	
	35 40 45	
55	gtc tat atc atg gcc gac aag cag aag aac ggc atc aag gtg aac ttc	192
	Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe	
	50 55 60	
60	aag atc cgc cac aac atc gag gac ggc agc gtg cag ctc gcc gac cac	240
	Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His	
	65 70 75 80	

YFP F2B Y203H mutation and Met added @ pos. 1  
SEQ ID NOS:274 & 275

	tac cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc gac	288
	Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp	
	85 90 95	
5	aac cac tac ctg agc cac cag tcc gcc ctg agc aaa gac ccc aac gag	336
	Asn His Tyr Leu Ser His Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu	
	100 105 110	
10	aag cgc gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg atc	384
	Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile	
	115 120 125	
15	act ctc ggc atg gac gag ctg tac aag	411
	Thr Leu Gly Met Asp Glu Leu Tyr Lys	
	130 135	
20	CFP F2B N146I mutation	
	SEQ ID NOS:276 & 277	
	gac ggc aac tac aag acc cgc gcc gag gtg aag ttc gag ggc gac acc	48
	Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr	
	1 5 10 15	
25	ctg gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag gac ggc	96
	Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly	
	20 25 30	
30	aac atc ctg ggg cac aag ctg gag tac aac tac atc agc cac aac gtc	144
	Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Ile Ser His Asn Val	
	35 40 45	
35	tat atc atg gcc gac aag cag aag aac ggc atc aag gtg aac ttc aag	192
	Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys	
	50 55 60	
40	atc cgc cac aac atc gag gac ggc agc gtg cag ctc gcc gac cac tac	240
	Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr	
	65 70 75 80	
45	cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc gac aac	288
	Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn	
	85 90 95	
	cac tac ctg agc acc cag tcc gcc ctg agc aaa gac ccc aac gag aag	336
	His Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys	
	100 105 110	
50	cgc gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg atc act	384
	Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr	
	115 120 125	
55	ctc ggc atg gac gag ctg tac aag	408
	Leu Gly Met Asp Glu Leu Tyr Lys	
	130 135	

CFP F2B N146I mutation and Met added @ pos. 1  
SEQ ID NOS:278 & 279

5	atg gac ggc aac tac aag acc cgc gcc gag gtg aag ttc gag ggc gac Met Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp 1 5 10 15	48
10	acc ctg gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag gac Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp 20 25 30	96
15	ggc aac atc ctg ggg cac aag ctg gag tac aac tac atc agc cac aac Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Ile Ser His Asn 35 40 45	144
20	gtc tat atc atg gcc gac aag cag aag aac ggc atc aag gtg aac ttc Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe 50 55 60	192
25	aag atc cgc cac aac atc gag gac ggc agc gtg cag ctc gcc gac cac Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His 65 70 75 80	240
30	tac cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc gac Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp 85 90 95	288
35	aac cac tac ctg agc acc cag tcc gcc ctg agc aaa gac ccc aac gag Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu 100 105 110	336
40	aag cgc gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg atc Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile 115 120 125	384
45	act ctc ggc atg gac gag ctg tac aag Thr Leu Gly Met Asp Glu Leu Tyr Lys 130 135	411

CFP F2B M153T mutation  
SEQ ID NOS:280 & 281

50	gac ggc aac tac aag acc cgc gcc gag gtg aag ttc gag ggc gac acc Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr 1 5 10 15	48
55	ctg gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag gac ggc Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly 20 25 30	96
60	aac atc ctg ggg cac aag ctg gag tac aac tac aac agc cac aac gtc Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val 35 40 45	144

	tat atc act gcc gac aag cag aag aac ggc atc aag gtg aac ttc aag	192
	Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys	
	50 55 60	
5		
	atc cgc cac aac atc gag gac ggc agc gtg cag ctc gcc gac cac tac	240
	Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr	
	65 70 75 80	
10		
	cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc gac aac	288
	Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn	
	85 90 95	
15		
	cac tac ctg agc acc cag tcc gcc ctg agc aaa gac ccc aac gag aag	336
	His Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys	
	100 105 110	
20		
	cgc gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg atc act	384
	Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr	
	115 120 125	
25		
	ctc ggc atg gac gag ctg tac aag	408
	Leu Gly Met Asp Glu Leu Tyr Lys	
	130 135	
	CFP F2B M153T mutation and Met added @ pos. 1	
	SEQ ID NOS:282 & 283	
30		
	atg gac ggc aac tac aag acc cgc gcc gag gtg aag ttc gag ggc gac	48
	Met Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp	
	1 5 10 15	
35		
	acc ctg gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag gac	96
	Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp	
	20 25 30	
40		
	ggc aac atc ctg ggg cac aag ctg gag tac aac tac aac agc cac aac	144
	Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn	
	35 40 45	
45		
	gtc tat atc act gcc gac aag cag aag aac ggc atc aag gtg aac ttc	192
	Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe	
	50 55 60	
50		
	aag atc cgc cac aac atc gag gac ggc agc gtg cag ctc gcc gac cac	240
	Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His	
	65 70 75 80	
55		
	tac cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc gac	288
	Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp	
	85 90 95	
55		
	aac cac tac ctg agc acc cag tcc gcc ctg agc aaa gac ccc aac gag	336
	Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu	
	100 105 110	



	aag cgc gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg atc	384
	Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile	
	115 120 125	
5	act ctc ggc atg gac gag ctg tac aag	411
	Thr Leu Gly Met Asp Glu Leu Tyr Lys	
	130 135	
10	CFP F2B N146I, M153T mutations	
	SEQ ID NOS:284 & 285	
	gac ggc aac tac aag acc cgc gcc gag gtg aag ttc gag ggc gac acc	48
	Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr	
15	1 5 10 15	
	ctg gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag gac ggc	96
	Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly	
	20 25 30	
20	aac atc ctg ggg cac aag ctg gag tac aac tac atc agc cac aac gtc	144
	Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Ile Ser His Asn Val	
	35 40 45	
25	tat atc acc gcc gac aag cag aag aac ggc atc aag gtg aac ttc aag	192
	Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys	
	50 55 60	
	atc cgc cac aac atc gag gac ggc agc gtg cag ctc gcc gac cac tac	240
	Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr	
30	65 70 75 80	
	cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc gac aac	288
	Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn	
35	85 90 95	
	cac tac ctg agc acc cag tcc gcc ctg agc aaa gac ccc aac gag aag	336
	His Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys	
	100 105 110	
40	cgc gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg atc act	384
	Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr	
	115 120 125	
45	ctc ggc atg gac gag ctg tac aag	408
	Leu Gly Met Asp Glu Leu Tyr Lys	
	130 135	
50	CFP F2B N146I,M153T mutations and Met added @ pos. 1	
	SEQ ID NOS:286 & 287	
	atg gac ggc aac tac aag acc cgc gcc gag gtg aag ttc gag ggc gac	48
	Met Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp	
55	1 5 10 15	

	acc ctg gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag gac	96
	Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp	
	20 25 30	
5	ggc aac atc ctg ggg cac aag ctg gag tac aac tac atc agc cac aac	144
	Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Ile Ser His Asn	
	35 40 45	
10	gtc tat atc acc gcc gac aag cag aag aac ggc atc aag gtg aac ttc	192
	Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe	
	50 55 60	
15	aag atc cgc cac aac atc gag gac ggc agc gtg cag ctc gcc gac cac	240
	Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His	
	65 70 75 80	
20	tac cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc gac	288
	Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp	
	85 90 95	
	aac cac tac ctg agc acc cag tcc gcc ctg agc aaa gac ccc aac gag	336
	Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu	
	100 105 110	
25	aag cgc gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg atc	384
	Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile	
	115 120 125	
30	act ctc ggc atg gac gag ctg tac aag	411
	Thr Leu Gly Met Asp Glu Leu Tyr Lys	
	130 135	
35	CFP F2B V163A mutation	
	SEQ ID NOS:288 & 289	
40	gac ggc aac tac aag acc cgc gcc gag gtg aag ttc gag ggc gac acc	48
	Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr	
	1 5 10 15	
45	ctg gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag gac ggc	96
	Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly	
	20 25 30	
	aac atc ctg ggg cac aag ctg gag tac aac tac aac agc cac aac gtc	144
	Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val	
	35 40 45	
50	tat atc atg gcc gac aag cag aag aac ggc atc aag gcc aac ttc aag	192
	Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Ala Asn Phe Lys	
	50 55 60	
55	atc cgc cac aac atc gag gac ggc agc gtg cag ctc gcc gac cac tac	240
	Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr	
	65 70 75 80	

	cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc gac aac	288
	Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn	
	85 90 95	
5	cac tac ctg agc acc cag tcc gcc ctg agc aaa gac ccc aac gag aag	336
	His Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys	
	100 105 110	
10	cgc gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg atc act	384
	Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr	
	115 120 125	
	ctc ggc atg gac gag ctg tac aag	408
15	Leu Gly Met Asp Glu Leu Tyr Lys	
	130 135	
CFP F2B V163A mutation and Met added @ posit. 1		
SEQ ID NOS:290 & 291		
20	atg gac ggc aac tac aag acc cgc gcc gag gtg aag ttc gag ggc gac	48
	Met Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp	
	1 5 10 15	
25	acc ctg gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag gac	96
	Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp	
	20 25 30	
30	ggc aac atc ctg ggg cac aag ctg gag tac aac tac aac agc cac aac	144
	Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn	
	35 40 45	
35	gtc tat atc atg gcc gac aag cag aag aac ggc atc aag gcc aac ttc	192
	Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Ala Asn Phe	
	50 55 60	
	aag atc cgc cac aac atc gag gac ggc agc gtg cag ctc gcc gac cac	240
	Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His	
	65 70 75 80	
40	tac cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc gac	288
	Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp	
	85 90 95	
45	aac cac tac ctg agc acc cag tcc gcc ctg agc aaa gac ccc aac gag	336
	Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu	
	100 105 110	
50	aag cgc gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg atc	384
	Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile	
	115 120 125	
55	act ctc ggc atg gac gag ctg tac aag	411
	Thr Leu Gly Met Asp Glu Leu Tyr Lys	
	130 135	

CFP F2B N146I,V163A mutations  
SEQ ID NOS:292 & 293

5	gac ggc aac tac aag acc cgc gcc gag gtg aag ttc gag ggc gac acc Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr 1 5 10 15	48
10	ctg gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag gac ggc Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly 20 25 30	96
15	aac atc ctg ggg cac aag ctg gag tac aac tac atc agc cac aac gtc Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Ile Ser His Asn Val 35 40 45	144
20	tat atc atg gcc gac aag cag aag aac ggc atc aag gcc aac ttc aag Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Ala Asn Phe Lys 50 55 60	192
25	atc cgc cac aac atc gag gac ggc agc gtg cag ctc gcc gac cac tac Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr 65 70 75 80	240
30	cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc gac aac Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn 85 90 95	288
35	cac tac ctg agc act cag tcc gcc ctg agc aaa gac ccc aac gag aag His Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys 100 105 110	336
40	cgc gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg atc act Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr 115 120 125	384
45	ctc ggc atg gac gag ctg tac aag Leu Gly Met Asp Glu Leu Tyr Lys 130 135	408

CFP F2B N146I,V163A mutations and Met added @ pos. 1  
SEQ ID NOS:294 & 295

45	atg gac ggc aac tac aag acc cgc gcc gag gtg aag ttc gag ggc gac Met Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp 1 5 10 15	48
50	acc ctg gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag gac Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp 20 25 30	96
55	ggc aac atc ctg ggg cac aag ctg gag tac aac tac atc agc cac aac Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Ile Ser His Asn 35 40 45	144

	gtc tat atc atg gcc gac aag cag aag aac ggc atc aag gcc aac ttc	192
	Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Ala Asn Phe	
	50 55 60	
5	aag atc cgc cac aac atc gag gac ggc agc gtg cag ctc gcc gac cac	240
	Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His	
	65 70 75 80	
10	tac cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc gac	288
	Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp	
	85 90 95	
15	aac cac tac ctg agc act cag tcc gcc ctg agc aaa gac ccc aac gag	336
	Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu	
	100 105 110	
20	aag cgc gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg atc	384
	Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile	
	115 120 125	
25	act ctc ggc atg gac gag ctg tac aag	411
	Thr Leu Gly Met Asp Glu Leu Tyr Lys	
	130 135	
30	CFP F2B M153T,V163A mutations SEQ ID NOS:296 & 297	
	gac ggc aac tac aag acc cgc gcc gag gtg aag ttc gag ggc gac acc	48
	Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr	
	1 5 10 15	
35	ctg gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag gac ggc	96
	Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly	
	20 25 30	
40	aac atc ctg ggc cac aag ctg gag tac aac tac aac agc cac aac gtc	144
	Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val	
	35 40 45	
45	tat atc acc gcc gac aag cag aag aac ggc atc aag gcc aac ttc aag	192
	Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly Ile Lys Ala Asn Phe Lys	
	50 55 60	
50	atc cgc cac aac atc gag gac ggc agc gtg cag ctc gcc gac cac tac	240
	Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr	
	65 70 75 80	
55	cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc gac aac	288
	Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn	
	85 90 95	
55	cac tac ctg agc act cag tcc gcc ctg agc aaa gac ccc aac gag aag	336
	His Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys	
	100 105 110	

	cgc gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg atc act	384
	Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr	
	115 120 125	
5	ctc ggc atg gac gag ctg tac aag	408
	Leu Gly Met Asp Glu Leu Tyr Lys	
	130 135	
10	CFP F2B,M153T,V163A mutations and Met added @ pos. 1	
	SEQ ID NOS:298 & 299	
15	atg gac ggc aac tac aag acc cgc gcc gag gtg aag ttc gag ggc gac	48
	Met Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp	
	1 5 10 15	
20	acc ctg gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag gac	96
	Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp	
	20 25 30	
25	ggc aac atc ctg ggg cac aag ctg gag tac aac tac aac agc cac aac	144
	Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn	
	35 40 45	
30	gtc tat atc acc gcc gac aag cag aag aac ggc atc aag gcc aac ttc	192
	Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly Ile Lys Ala Asn Phe	
	50 55 60	
35	aag atc cgc cac aac atc gag gac ggc agc gtg cag ctc gcc gac cac	240
	Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His	
	65 70 75 80	
40	tac cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc gac	288
	Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp	
	85 90 95	
45	aac cac tac ctg agc act cag tcc gcc ctg agc aaa gac ccc aac gag	336
	Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu	
	100 105 110	
50	aag cgc gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg atc	384
	Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile	
	115 120 125	
55	act ctc ggc atg gac gag ctg tac aag	411
	Thr Leu Gly Met Asp Glu Leu Tyr Lys	
	130 135	
50	CFP F2B , N146I,M153T,and V163A mutations	
	SEQ ID NOS:300 & 301	
55	gac ggc aac tac aag acc cgc gcc gag gtg aag ttc gag ggc gac acc	48
	Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr	
	1 5 10 15	

	ctg gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag gac ggc	96
	Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly	
	20 25 30	
5	aac atc ctg ggg cac aag ctg gag tac aac tac atc agc cac aac gtc	144
	Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Ile Ser His Asn Val	
	35 40 45	
10	tat atc acc gcc gac aag cag aag aac ggc atc aag gcc aac ttc aag	192
	Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly Ile Lys Ala Asn Phe Lys	
	50 55 60	
15	atc cgc cac aac atc gag gac ggc agc gtg cag ctc gcc gac cac tac	240
	Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr	
	65 70 75 80	
20	cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc gac aac	288
	Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn	
	85 90 95	
	cac tac ctg agc acc cag tcc gcc ctg agc aaa gac ccc aac gag aag	336
	His Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys	
	100 105 110	
25	cgc gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg atc act	384
	Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr	
	115 120 125	
30	ctc ggc atg gac gag ctg tac aag	408
	Leu Gly Met Asp Glu Leu Tyr Lys	
	130 135	
35	CFP F2B , N146I,M153T,and V163A mutations and Met added @ pos. 1 SEQ ID NOS:302 & 303	
40	atg gac ggc aac tac aag acc cgc gcc gag gtg aag ttc gag ggc gac	48
	Met Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp	
	1 5 10 15	
45	acc ctg gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag gac	96
	Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp	
	20 25 30	
50	ggc aac atc ctg ggg cac aag ctg gag tac aac tac atc agc cac aac	144
	Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Ile Ser His Asn	
	35 40 45	
	gtc tat atc acc gcc gac aag cag aag aac ggc atc aag gcc aac ttc	192
	Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly Ile Lys Ala Asn Phe	
	50 55 60	
55	aag atc cgc cac aac atc gag gac ggc agc gtg cag ctc gcc gac cac	240
	Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His	
	65 70 75 80	

	tac cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc gac	288
	Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp	
	85 90 95	
5	aac cac tac ctg agc acc cag tcc gcc ctg agc aaa gac ccc aac gag	336
	Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu	
	100 105 110	
10	aag cgc gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg atc	384
	Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile	
	115 120 125	
	act ctc ggc atg gac gag ctg tac aag	411
15	Thr Leu Gly Met Asp Glu Leu Tyr Lys	
	130 135	
20	CGFP F2B , N146I, T203Y mutations SEQ ID NOS:304 & 305	
	gac ggc aac tac aag acc cgc gcc gag gtg aag ttc gag ggc gac acc	48
	Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr	
	1 5 10 15	
25	ctg gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag gac ggc	96
	Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly	
	20 25 30	
30	aac atc ctg ggg cac aag ctg gag tac aac tac atc agc cac aac gtc	144
	Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Ile Ser His Asn Val	
	35 40 45	
	tat atc atg gcc gac aag cag aag aac ggc atc aag gtg aac ttc aag	192
35	Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys	
	50 55 60	
	atc cgc cac aac atc gag gac ggc agc gtg cag ctc gcc gac cac tac	240
	Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr	
40	65 70 75 80	
	cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc gac aac	288
	Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn	
	85 90 95	
45	cac tac ctg agc tac cag tcc gcc ctg agc aaa gac ccc aac gag aag	336
	His Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys	
	100 105 110	
50	cgc gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg atc act	384
	Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr	
	115 120 125	
	ctc ggc atg gac gag ctg tac aag	408
55	Leu Gly Met Asp Glu Leu Tyr Lys	
	130 135	



CGFP F2B , N146I,T203Y mutations and Met added @ pos. 1  
SEQ ID NOS:306 & 307

5	atg gac ggc aac tac aag acc cgc gcc gag gtg aag ttc gag ggc gac Met Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp 1 5 10 15	48
10	acc ctg gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag gac Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp 20 25 30	96
15	ggc aac atc ctg ggg cac aag ctg gag tac aac tac atc agc cac aac Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Ile Ser His Asn 35 40 45	144
20	gtc tat atc atg gcc gac aag cag aag aac ggc atc aag gtg aac ttc Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe 50 55 60	192
25	aag atc cgc cac aac atc gag gac ggc agc gtg cag ctc gcc gac cac Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His 65 70 75 80	240
30	tac cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc gac Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp 85 90 95	288
35	aac cac tac ctg agc tac cag tcc gcc ctg agc aaa gac ccc aac gag Asn His Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu 100 105 110	336
40	aag cgc gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg atc Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile 115 120 125	384
45	act ctc ggc atg gac gag ctg tac aag Thr Leu Gly Met Asp Glu Leu Tyr Lys 130 135	411

CGFP F2B ,M153T, T203Y mutations  
SEQ ID NOS:308 & 309

45	gac ggc aac tac aag acc cgc gcc gag gtg aag ttc gag ggc gac acc Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr 1 5 10 15	48
50	ctg gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag gac ggc Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly 20 25 30	96
55	aac atc ctg ggg cac aag ctg gag tac aac tac aac agc cac aac gtc Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val 35 40 45	144

	tat atc acc gcc gac aag cag aag aac ggc atc aag gtg aac ttc aag	192
	Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys	
	50 55 60	
5	atc cgc cac aac atc gag gac ggc agc gtg cag ctc gcc gac cac tac	240
	Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr	
	65 70 75 80	
10	cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc gac aac	288
	Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn	
	85 90 95	
15	cac tac ctg agc tac cag tcc gcc ctg agc aaa gac ccc aac gag aag	336
	His Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys	
	100 105 110	
20	cgc gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg atc act	384
	Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr	
	115 120 125	
25	ctc ggc atg gac gag ctg tac aag	408
	Leu Gly Met Asp Glu Leu Tyr Lys	
	130 135	
30	CGFP F2B , M153T, T203Y mutations + Met @ posit. SEQ ID NOS:310 & 311	
35	atg gac ggc aac tac aag acc cgc gcc gag gtg aag ttc gag ggc gac	48
	Met Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp	
	1 5 10 15	
40	acc ctg gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag gac	96
	Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp	
	20 25 30	
45	ggc aac atc ctg ggg cac aag ctg gag tac aac tac aac agc cac aac	144
	Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn	
	35 40 45	
50	gtc tat atc acc gcc gac aag cag aag aac ggc atc aag gtg aac ttc	192
	Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe	
	50 55 60	
55	aag atc cgc cac aac atc gag gac ggc agc gtg cag ctc gcc gac cac	240
	Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His	
	65 70 75 80	
60	tac cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc gac	288
	Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp	
	85 90 95	
65	aac cac tac ctg agc tac cag tcc gcc ctg agc aaa gac ccc aac gag	336
	Asn His Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu	
	100 105 110	

	aag cgc gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg atc	384
	Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile	
	115 120 125	
5		
	act ctc ggc atg gac gag ctg tac aag	411
	Thr Leu Gly Met Asp Glu Leu Tyr Lys	
	130 135	
10	CGFP F2B, N146I, M153T, and T203Y mutations	
	SEQ ID NOS:312 & 313	
	gac ggc aac tac aag acc cgc gcc gag gtg aag ttc gag ggc gac acc	48
	Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr	
15	1 5 10 15	
	ctg gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag gac ggc	96
	Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly	
	20 25 30	
20		
	aac atc ctg ggg cac aag ctg gag tac aac tac atc agc cac aac gtc	144
	Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Ile Ser His Asn Val	
	35 40 45	
25		
	tat atc acc gcc gac aag cag aag aac ggc atc aag gtg aac ttc aag	192
	Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys	
	50 55 60	
	atc cgc cac aac atc gag gac ggc agc gtg cag ctc gcc gac cac tac	240
	Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr	
30	65 70 75 80	
	cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc gac aac	288
	Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn	
35	85 90 95	
	cac tac ctg agc tac cag tcc gcc ctg agc aaa gac ccc aac gag aag	336
	His Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys	
	100 105 110	
40		
	cgc gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg atc act	384
	Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr	
	115 120 125	
45		
	ctc ggc atg gac gag ctg tac aag	408
	Leu Gly Met Asp Glu Leu Tyr Lys	
	130 135	
50		
	CGFP F2B, N146I, M153T, and T203Y mutations and Met added @ pos. 1	
	SEQ ID NOS:314 & 315	
	atg gac ggc aac tac aag acc cgc gcc gag gtg aag ttc gag ggc gac	48
	Met Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp	
55	1 5 10 15	

	acc ctg gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag gac	96
	Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp	
	20 25 30	
5	ggc aac atc ctg ggg cac aag ctg gag tac aac tac atc agc cac aac	144
	Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Ile Ser His Asn	
	35 40 45	
10	gtc tat atc acc gcc gac aag cag aag aac ggc atc aag gtg aac ttc	192
	Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe	
	50 55 60	
15	aag atc cgc cac aac atc gag gac ggc agc gtg cag ctc gcc gac cac	240
	Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His	
	65 70 75 80	
20	tac cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc gac	288
	Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp	
	85 90 95	
25	aac cac tac ctg agc tac cag tcc gcc ctg agc aaa gac ccc aac gag	336
	Asn His Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu	
	100 105 110	
30	aag cgc gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg atc	384
	Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile	
	115 120 125	
35	act ctc ggc atg gac gag ctg tac aag	411
	Thr Leu Gly Met Asp Glu Leu Tyr Lys	
	130 135	
40	CGFP F2B , V163A, T203Y mutations	
	SEQ ID NOS:316 & 317	
45	gac ggc aac tac aag acc cgc gcc gag gtg aag ttc gag ggc gac acc	48
	Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr	
	1 5 10 15	
50	ctg gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag gac ggc	96
	Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly	
	20 25 30	
55	aac atc ctg ggg cac aag ctg gag tac aac tac aac agc cac aac gtc	144
	Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val	
	35 40 45	
60	tat atc atg gcc gac aag cag aag aac ggc atc aag gcc aac ttc aag	192
	Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Ala Asn Phe Lys	
	50 55 60	
65	atc cgc cac aac atc gag gac ggc agc gtg cag ctc gcc gac cac tac	240
	Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr	
	65 70 75 80	

	cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc gac aac	288
	Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn	
	85 90 95	
5	cac tac ctg agc tac cag tcc gcc ctg agc aaa gac ccc aac gag aag	336
	His Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys	
	100 105 110	
10	cgc gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg atc act	384
	Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr	
	115 120 125	
15	ctc ggc atg gac gag ctg tac aag	408
	Leu Gly Met Asp Glu Leu Tyr Lys	
	130 135	
20	CGFP F2B , V163A, T203Y mutations and Met added @ pos. 1	
	SEQ ID NOS:318 & 319	
	atg gac ggc aac tac aag acc cgc gcc gag gtg aag ttc gag ggc gac	48
	Met Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp	
	1 5 10 15	
25	acc ctg gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag gac	96
	Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp	
	20 25 30	
30	ggc aac atc ctg ggg cac aag ctg gag tac aac tac aac agc cac aac	144
	Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn	
	35 40 45	
35	gtc tat atc atg gcc gac aag cag aag aac ggc atc aag gcc aac ttc	192
	Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Ala Asn Phe	
	50 55 60	
40	aag atc cgc cac aac atc gag gac ggc agc gtg cag ctc gcc gac cac	240
	Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His	
	65 70 75 80	
	tac cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc gac	288
	Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp	
	85 90 95	
45	aac cac tac ctg agc tac cag tcc gcc ctg agc aaa gac ccc aac gag	336
	Asn His Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu	
	100 105 110	
50	aag cgc gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg atc	384
	Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile	
	115 120 125	
55	act ctc ggc atg gac gag ctg tac aag	411
	Thr Leu Gly Met Asp Glu Leu Tyr Lys	
	130 135	

CGFP F2B, N146I, V163A, and T203Y mutations  
SEQ ID NOS:320 & 321

5	gac ggc aac tac aag acc cgc gcc gag gtg aag ttc gag ggc gac acc Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr 1 5 10 15	48
10	ctg gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag gac ggc Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly 20 25 30	96
15	aac atc ctg ggg cac aag ctg gag tac aac tac atc agc cac aac gtc Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Ile Ser His Asn Val 35 40 45	144
20	tat atc atg gcc gac aag cag aag aac ggc atc aag gcc aac ttc aag Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Ala Asn Phe Lys 50 55 60	192
25	atc cgc cac aac atc gag gac ggc agc gtg cag ctc gcc gac cac tac Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr 65 70 75 80	240
30	cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc gac aac Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn 85 90 95	288
35	cac tac ctg agc tac cag tcc gcc ctg agc aaa gac ccc aac gag aag His Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys 100 105 110	336
40	cgc gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg atc act Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Glu Ile Thr 115 120 125	384
45	ctc ggc atg gac gag ctg tac aag Leu Gly Met Asp Glu Leu Tyr Lys 130 135	408

CGFP F2B, N146I, V163A, and T203Y mutations and Met added @ pos. 1  
SEQ ID NOS:322 & 323

45	atg gac ggc aac tac aag acc cgc gcc gag gtg aag ttc gag ggc gac Met Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp 1 5 10 15	48
50	acc ctg gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag gac Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp 20 25 30	96
55	ggc aac atc ctg ggg cac aag ctg gag tac aac tac atc agc cac aac Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Ile Ser His Asn 35 40 45	144

	gtc tat atc atg gcc gac aag cag aag aac ggc atc aag gcc aac ttc	192
	Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Ala Asn Phe	
	50 55 60	
5	aag atc cgc cac aac atc gag gac ggc agc gtg cag ctc gcc gac cac	240
	Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His	
	65 70 75 80	
10	tac cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc gac	288
	Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp	
	85 90 95	
15	aac cac tac ctg agc tac cag tcc gcc ctg agc aaa gac ccc aac gag	336
	Asn His Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu	
	100 105 110	
20	aag cgc gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg atc	384
	Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile	
	115 120 125	
25	act ctc ggc atg gac gag ctg tac aag	411
	Thr Leu Gly Met Asp Glu Leu Tyr Lys	
	130 135	
30	CGFP F2B, M153T, V163A, and T203Y mutations SEQ ID NOS:324 & 325	
	gac ggc aac tac aag acc cgc gcc gag gtg aag ttc gag ggc gac acc	48
	Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr	
	1 5 10 15	
35	ctg gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag gac ggc	96
	Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly	
	20 25 30	
40	aac atc ctg ggg cac aag ctg gag tac aac tac aac agc cac aac gtc	144
	Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val	
	35 40 45	
45	tat atc acc gcc gac aag cag aag aac ggc atc aag gcc aac ttc aag	192
	Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly Ile Lys Ala Asn Phe Lys	
	50 55 60	
50	atc cgc cac aac atc gag gac ggc agc gtg cag ctc gcc gac cac tac	240
	Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr	
	65 70 75 80	
55	cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc gac aac	288
	Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn	
	85 90 95	
55	cac tac ctg agc tac cag tcc gcc ctg agc aaa gac ccc aac gag aag	336
	His Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys	
	100 105 110	

	cgc gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg atc act	384
	Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr	
	115 120 125	
5		
	ctc ggc atg gac gag ctg tac aag	408
	Leu Gly Met Asp Glu Leu Tyr Lys	
	130 135	
10		
	CGFP F2B, M153T,V163A,and T203Y mutations and Met added @ pos. 1 SEQ ID NOS:326 & 327	
15	atg gac ggc aac tac aag acc cgc gcc gag gtg aag ttc gag ggc gac	48
	Met Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp	
	1 5 10 15	
20	acc ctg gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag gac	96
	Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp	
	20 25 30	
25	ggc aac atc ctg ggg cac aag ctg gag tac aac tac aac agc cac aac	144
	Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn	
	35 40 45	
30	gtc tat atc acc gcc gac aag cag aag aac ggc atc aag gcc aac ttc	192
	Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly Ile Lys Ala Asn Phe	
	50 55 60	
35	aag atc cgc cac aac atc gag gac ggc agc gtg cag ctc gcc gac cac	240
	Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His	
	65 70 75 80	
40	tac cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc gac	288
	Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp	
	85 90 95	
45	aac cac tac ctg agc tac cag tcc gcc ctg agc aaa gac ccc aac gag	336
	Asn His Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu	
	100 105 110	
50	aag cgc gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg atc	384
	Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile	
	115 120 125	
55	act ctc ggc atg gac gag ctg tac aag	411
	Thr Leu Gly Met Asp Glu Leu Tyr Lys	
	130 135	
50		
	CGFP F2B, N146I,M153T,V163A,and T203Y mutations SEQ ID NOS:328 & 329	
55	gac ggc aac tac aag acc cgc gcc gag gtg aag ttc gag ggc gac acc	48
	Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr	
	1 5 10 15	



	ctg gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag gac ggc	96
	Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly	
	20 25 30	
5	aac atc ctg ggg cac aag ctg gag tac aac tac atc agc cac aac gtc	144
	Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Ile Ser His Asn Val	
	35 40 45	
10	tat atc acc gcc gac aag cag aag aac ggc atc aag gcc aac ttc aag	192
	Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly Ile Lys Ala Asn Phe Lys	
	50 55 60	
15	atc cgc cac aac atc gag gac ggc agc gtg cag ctc gcc gac cac tac	240
	Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr	
	65 70 75 80	
20	cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc gac aac	288
	Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn	
	85 90 95	
25	cac tac ctg agc tac cag tcc gcc ctg agc aaa gac ccc aac gag aag	336
	His Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys	
	100 105 110	
30	cgc gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg atc act	384
	Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr	
	115 120 125	
35	ctc ggc atg gac gag ctg tac aag	408
	Leu Gly Met Asp Glu Leu Tyr Lys	
	130 135	
40	CGFP F2B, N146I,M153T,V163A,and T203Y mutations and Met added @ pos. 1 SEQ ID NOS:330 & 331	
45	atg gac ggc aac tac aag acc cgc gcc gag gtg aag ttc gag ggc gac	48
	Met Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp	
	1 5 10 15	
50	acc ctg gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag gac	96
	Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp	
	20 25 30	
55	ggc aac atc ctg ggg cac aag ctg gag tac aac tac atc agc cac aac	144
	Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Ile Ser His Asn	
	35 40 45	
60	gtc tat atc acc gcc gac aag cag aag aac ggc atc aag gcc aac ttc	192
	Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly Ile Lys Ala Asn Phe	
	50 55 60	
65	aag atc cgc cac aac atc gag gac ggc agc gtg cag ctc gcc gac cac	240
	Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His	
	65 70 75 80	

	tac cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc gac	288
	Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp	
	85 90 95	
5	aac cac tac ctg agc tac cag tcc gcc ctg agc aaa gac ccc aac gag	336
	Asn His Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu	
	100 105 110	
10	aag cgc gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg atc	384
	Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile	
	115 120 125	
15	act ctc ggc atg gac gag ctg tac aag	411
	Thr Leu Gly Met Asp Glu Leu Tyr Lys	
	130 135	
20	BFP F2B, Y145F mutation SEQ ID NOS:332 & 333	
	gac ggc aac tac aag acc cgc gcc gag gtg aag ttc gag ggc gac acc	48
	Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr	
	1 5 10 15	
25	ctg gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag gac ggc	96
	Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly	
	20 25 30	
30	aac atc ctg ggg cac aag ctg gag tac aac ttc aac agc cac aac gtc	144
	Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Phe Asn Ser His Asn Val	
	35 40 45	
35	tat atc atg gcc gac aag cag aag aac ggc atc aag gtg aac ttc aag	192
	Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys	
	50 55 60	
40	atc cgc cac aac atc gag gac ggc agc gtg cag ctc gcc gac cac tac	240
	Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr	
	65 70 75 80	
45	cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc gac aac	288
	Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn	
	85 90 95	
	cac tac ctg agc acc cag tcc gcc ctg agc aaa gac ccc aac gag aag	336
	His Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys	
	100 105 110	
50	cgc gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg atc act	384
	Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr	
	115 120 125	
55	ctc ggc atg gac gag ctg tac aag	408
	Leu Gly Met Asp Glu Leu Tyr Lys	
	130 135	

BFP F2B, Y145F mutation and Met added @ pos. 1

SEQ ID NOS:334 & 335

5	atg gac ggc aac tac aag acc cgc gcc gag gtg aag ttc gag ggc gac	48
	Met Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp	
	1 5 10 15	
10	acc ctg gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag gac	96
	Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp	
	20 25 30	
15	ggc aac atc ctg ggg cac aag ctg gag tac aac ttc aac agc cac aac	144
	Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Phe Asn Ser His Asn	
	35 40 45	
20	gtc tat atc atg gcc gac aag cag aag aac ggc atc aag gtg aac ttc	192
	Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe	
	50 55 60	
25	aag atc cgc cac aac atc gag gac ggc agc gtg cag ctc gcc gac cac	240
	Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His	
	65 70 75 80	
30	tac cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc gac	288
	Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp	
	85 90 95	
35	aac cac tac ctg agc acc cag tcc gcc ctg agc aaa gac ccc aac gag	336
	Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu	
	100 105 110	
40	aag cgc gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggc atc	384
	Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile	
	115 120 125	
45	act ctc ggc atg gac gag ctg tac aag	411
	Thr Leu Gly Met Asp Glu Leu Tyr Lys	
	130 135	

Venus F2B, S175G mutation

SEQ ID NOS:336 & 337

45	gac ggc aac tac aag acc cgc gcc gag gtg aag ttc gag ggc gac acc	48
	Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr	
	1 5 10 15	
50	ctg gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag gac ggc	96
	Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly	
	20 25 30	
55	aac atc ctg ggg cac aag ctg gag tac aac tac aac agc cac aac gtc	144
	Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val	
	35 40 45	

	tat atc atg gcc gac aag cag aag aac ggc atc aag gtg aac ttc aag	192
	Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys	
	50 55 60	
5		
	atc cgc cac aac atc gag gac ggc ggc gtg cag ctc gcc gac cac tac	240
	Ile Arg His Asn Ile Glu Asp Gly Gly Val Gln Leu Ala Asp His Tyr	
	65 70 75 80	
10		
	cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc gac aac	288
	Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn	
	85 90 95	
15		
	cac tac ctg agc tac cag tcc gcc ctg agc aaa gac ccc aac gag aag	336
	His Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys	
	100 105 110	
20		
	cgc gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg atc act	384
	Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr	
	115 120 125	
25		
	ctc ggc atg gac gag ctg tac aag	408
	Leu Gly Met Asp Glu Leu Tyr Lys	
	130 135	
	Venus F2B,S175G mutation and Met added @ pos. 1	
	SEQ ID NOS:338 & 339	
30		
	atg gac ggc aac tac aag acc cgc gcc gag gtg aag ttc gag ggc gac	48
	Met Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp	
	1 5 10 15	
35		
	acc ctg gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag gac	96
	Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp	
	20 25 30	
40		
	ggc aac atc ctg ggg cac aag ctg gag tac aac tac aac agc cac aac	144
	Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn	
	35 40 45	
45		
	gtc tat atc atg gcc gac aag cag aag aac ggc atc aag gtg aac ttc	192
	Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe	
	50 55 60	
50		
	aag atc cgc cac aac atc gag gac ggc ggc gtg cag ctc gcc gac cac	240
	Lys Ile Arg His Asn Ile Glu Asp Gly Gly Val Gln Leu Ala Asp His	
	65 70 75 80	
55		
	tac cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc gac	288
	Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp	
	85 90 95	
55		
	aac cac tac ctg agc tac cag tcc gcc ctg agc aaa gac ccc aac gag	336
	Asn His Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu	
	100 105 110	

	aag cgc gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg atc	384
	Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile	
	115 120 125	
5	act ctc ggc atg gac gag ctg tac aag	411
	Thr Leu Gly Met Asp Glu Leu Tyr Lys	
	130 135	
10	Venus F2B, M153T, S175G mutations	
	SEQ ID NOS:340 & 341	
	gac ggc aac tac aag acc cgc gcc gag gtg aag ttc gag ggc gac acc	48
	Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr	
15	1 5 10 15	
	ctg gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag gac ggc	96
	Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly	
	20 25 30	
20	aac atc ctg ggc cac aag ctg gag tac aac tac aac agc cac aac gtc	144
	Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val	
	35 40 45	
25	tat atc acc gcc gac aag cag aag aac ggc atc aag gtg aac ttc aag	192
	Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys	
	50 55 60	
	atc cgc cac aac atc gag gac ggc ggc gtg cag ctc gcc gac cac tac	240
30	Ile Arg His Asn Ile Glu Asp Gly Gly Val Gln Leu Ala Asp His Tyr	
	65 70 75 80	
	cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc gac aac	288
	Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn	
35	85 90 95	
	cac tac ctg agc tac cag tcc gcc ctg agc aaa gac ccc aac gag aag	336
	His Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys	
	100 105 110	
40	cgc gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg atc act	384
	Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr	
	115 120 125	
45	ctc ggc atg gac gag ctg tac aag	408
	Leu Gly Met Asp Glu Leu Tyr Lys	
	130 135	
50	Venus F2B, M153T, S175G mutations and Met added @ pos. 1	
	SEQ ID NOS:342 & 343	
55	atg gac ggc aac tac aag acc cgc gcc gag gtg aag ttc gag ggc gac	48
	Met Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp	
	1 5 10 15	

	acc ctg gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag gac	96
	Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp	
	20 25 30	
5	ggc aac atc ctg ggg cac aag ctg gag tac aac tac aac agc cac aac	144
	Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn	
	35 40 45	
10	gtc tat atc acc gcc gac aag cag aag aac ggc atc aag gtg aac ttc	192
	Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe	
	50 55 60	
15	aag atc cgc cac aac atc gag gac ggc ggc gtg cag ctc gcc gac cac	240
	Lys Ile Arg His Asn Ile Glu Asp Gly Gly Val Gln Leu Ala Asp His	
	65 70 75 80	
20	tac cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc gac	288
	Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp	
	85 90 95	
25	aac cac tac ctg agc tac cag tcc gcc ctg agc aaa gac ccc aac gag	336
	Asn His Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu	
	100 105 110	
30	aag cgc gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg atc	384
	Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile	
	115 120 125	
35	act ctc ggc atg gac gag ctg tac aag	411
	Thr Leu Gly Met Asp Glu Leu Tyr Lys	
	130 135	
35	Venus F2B, V163A,S175G mutations SEQ ID NOS:344 & 345	
40	gac ggc aac tac aag acc cgc gcc gag gtg aag ttc gag ggc gac acc	48
	Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr	
	1 5 10 15	
45	ctg gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag gac ggc	96
	Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly	
	20 25 30	
50	aac atc ctg ggg cac aag ctg gag tac aac tac aac agc cac aac gtc	144
	Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val	
	35 40 45	
55	tat atc atg gcc gac aag cag aag aac ggc atc aag gcc aac ttc aag	192
	Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Ala Asn Phe Lys	
	50 55 60	
55	atc cgc cac aac atc gag gac ggc ggc gtg cag ctc gcc gac cac tac	240
	Ile Arg His Asn Ile Glu Asp Gly Gly Val Gln Leu Ala Asp His Tyr	
	65 70 75 80	

	cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc gac aac	288
	Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn	
	85 90 95	
5	cac tac ctg agc tac cag tcc gcc ctg agc aaa gac ccc aac gag aag	336
	His Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys	
	100 105 110	
10	cgc gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg atc act	384
	Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr	
	115 120 125	
15	ctc ggc atg gac gag ctg tac aag	408
	Leu Gly Met Asp Glu Leu Tyr Lys	
	130 135	
20	Venus F2B, V163A,S175G mutations and Met added @ pos. 1 SEQ ID NOS:346 & 347	
25	atg gac ggc aac tac aag acc cgc gcc gag gtg aag ttc gag ggc gac	48
	Met Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp	
	1 5 10 15	
25	acc ctg gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag gac	96
	Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp	
	20 25 30	
30	ggc aac atc ctg ggg cac aag ctg gag tac aac tac aac agc cac aac	144
	Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn	
	35 40 45	
35	gtc tat atc atg gcc gac aag cag aag aac ggc atc aag gcc aac ttc	192
	Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Ala Asn Phe	
	50 55 60	
40	aag atc cgc cac aac atc gag gac ggc ggc gtg cag ctc gcc gac cac	240
	Lys Ile Arg His Asn Ile Glu Asp Gly Gly Val Gln Leu Ala Asp His	
	65 70 75 80	
45	tac cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc gac	288
	Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp	
	85 90 95	
45	aac cac tac ctg agc tac cag tcc gcc ctg agc aaa gac ccc aac gag	336
	Asn His Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu	
	100 105 110	
50	aag cgc gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg atc	384
	Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile	
	115 120 125	
55	act ctc ggc atg gac gag ctg tac aag	411
	Thr Leu Gly Met Asp Glu Leu Tyr Lys	
	130 135	

Venus F2B, M153T, V163A, S175G mutations  
SEQ ID NOS:348 & 349

5	gac ggc aac tac aag acc cgc gcc gag gtg aag ttc gag ggc gac acc Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr 1 5 10 15	48
10	ctg gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag gac ggc Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly 20 25 30	96
15	aac atc ctg ggg cac aag ctg gag tac aac tac aac agc cac aac gtc Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val 35 40 45	144
20	tat atc acc gcc gac aag cag aag aac ggc atc aag gcc aac ttc aag Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly Ile Lys Ala Asn Phe Lys 50 55 60	192
25	atc cgc cac aac atc gag gac ggc ggc gtg cag ctc gcc gac cac tac Ile Arg His Asn Ile Glu Asp Gly Gly Val Gln Leu Ala Asp His Tyr 65 70 75 80	240
30	cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc gac aac Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn 85 90 95	288
35	cac tac ctg agc tac cag tcc gcc ctg agc aaa gac ccc aac gag aag His Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys 100 105 110	336
40	cgc gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggc atc act Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr 115 120 125	384
45	ctc ggc atg gac gag ctg tac aag Leu Gly Met Asp Glu Leu Tyr Lys 130 135	408

Venus F2B, M153T, V163A, S175G mutations and Met added @ pos. 1  
SEQ ID NOS:350 & 351

50	atg gac ggc aac tac aag acc cgc gcc gag gtg aag ttc gag ggc gac Met Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp 1 5 10 15	48
55	acc ctg gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag gac Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp 20 25 30	96
60	ggc aac atc ctg ggg cac aag ctg gag tac aac tac aac agc cac aac Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn 35 40 45	144



	gtc tat atc acc gcc gac aag cag aag aac ggc atc aag gcc aac ttc	192
	Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly Ile Lys Ala Asn Phe	
	50 55 60	
5	aag atc cgc cac aac atc gag gac ggc ggc gtg cag ctc gcc gac cac	240
	Lys Ile Arg His Asn Ile Glu Asp Gly Gly Val Gln Leu Ala Asp His	
	65 70 75 80	
10	tac cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc gac	288
	Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp	
	85 90 95	
15	aac cac tac ctg agc tac cag tcc gcc ctg agc aaa gac ccc aac gag	336
	Asn His Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu	
	100 105 110	
20	aag cgc gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg atc	384
	Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile	
	115 120 125	
25	act ctc ggc atg gac gag ctg tac aag	411
	Thr Leu Gly Met Asp Glu Leu Tyr Lys	
	130 135	
YFP F1C (aa residues 1-117 of EYFP) with pos. 1 Met removed		
SEQ ID NOS:352 & 353		
30	gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc	48
	Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val	
	1 5 10 15	
35	gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag	96
	Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu	
	20 25 30	
40	ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc tgc	144
	Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys	
	35 40 45	
45	acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ttc	192
	Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe	
	50 55 60	
50	ggc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag cgg	240
	Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg	
	65 70 75 80	
55	cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc	288
	His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg	
	85 90 95	
55	acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag gtg	336
	Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val	
	100 105 110	

	aag ttc gag ggc	348
	Lys Phe Glu Gly	
	115	
5	YFP F1C, F46L mutation	
	SEQ ID NOS:354 & 355	
10	atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg	48
	Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu	
	1 5 10 15	
15	gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc	96
	Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly	
	20 25 30	
20	gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ctg atc	144
	Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Leu Ile	
	35 40 45	
25	tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc	192
	Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr	
	50 55 60	
30	ttc ggc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag	240
	Phe Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys	
	65 70 75 80	
35	cgg cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag	288
	Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu	
	85 90 95	
40	cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag	336
	Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu	
	100 105 110	
45	gtg aag ttc gag ggc	351
	Val Lys Phe Glu Gly	
	115	
50	YFP F1C, F46L mutation and pos. 1 Met removed	
	SEQ ID NOS:356 & 357	
55	gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc	48
	Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val	
	1 5 10 15	
60	gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag	96
	Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu	
	20 25 30	
65	ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ctg atc tgc	144
	Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Leu Ile Cys	
	35 40 45	

	acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ttc	192
	Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe	
	50 55 60	
5	ggc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag cgg	240
	Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg	
	65 70 75 80	
10	cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc	288
	His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg	
	85 90 95	
15	acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag gtg	336
	Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val	
	100 105 110	
	aag ttc gag ggc	348
	Lys Phe Glu Gly	
	115	
20		
	YFP F1C, K79R mutation	
	SEQ ID NOS:358 & 359	
25	atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg	48
	Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu	
	1 5 10 15	
30	gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc	96
	Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly	
	20 25 30	
35	gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc	144
	Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile	
	35 40 45	
	tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc	192
	Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr	
	50 55 60	
40		
	ttc ggc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg cgc	240
	Phe Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Arg	
	65 70 75 80	
45	cgg cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag	288
	Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu	
	85 90 95	
50	cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag	336
	Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu	
	100 105 110	
	gtg aag ttc gag ggc	351
	Val Lys Phe Glu Gly	
	115	
55		

YFP F1C, K79R mutation and pos. 1 Met removed  
SEQ ID NOS:360 & 361

5	gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val 1 5 10 15	48
10	gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu 20 25 30	96
15	ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc tgc Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys 35 40 45	144
20	acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ttc Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe 50 55 60	192
25	ggc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg cgc cgg Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Arg Arg 65 70 75 80	240
30	cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg 85 90 95	288
35	acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag gtg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val 100 105 110	336
40	aag ttc gag ggc Lys Phe Glu Gly 115	348

YFP F1C, Y66F mutation  
SEQ ID NOS:362 & 363

45	atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu 1 5 10 15	48
50	gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly 20 25 30	96
55	gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile 35 40 45	144
60	tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr 50 55 60	192

	ttc ggc ttc ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag	240
	Phe Gly Phe Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys	
	65 70 75 80	
5	cgg cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag	288
	Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu	
	85 90 95	
10	cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag	336
	Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu	
	100 105 110	
	gtg aag ttc gag ggc	351
15	Val Lys Phe Glu Gly	
	115	
20	YFP F1C, Y66F mutation and pos.1 Met removed SEQ ID NOS:364 & 365	
	gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc	48
	Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val	
	1 5 10 15	
25	gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag	96
	Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu	
	20 25 30	
30	ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc tgc	144
	Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys	
	35 40 45	
35	acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ttc	192
	Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe	
	50 55 60	
40	ggc ttc ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag cgg	240
	Gly Phe Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg	
	65 70 75 80	
	cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc	288
	His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg	
	85 90 95	
45	acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag gtg	336
	Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val	
	100 105 110	
50	aag ttc gag ggc	348
	Lys Phe Glu Gly	
	115	
55	YFP F1C, Q69K mutation SEQ ID NOS:366 & 367	

	atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg	48
	Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu	
	1 5 10 15	
5	gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc	96
	Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly	
	20 25 30	
10	gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc	144
	Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile	
	35 40 45	
15	tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc	192
	Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr	
	50 55 60	
20	ttc ggc tac ggc ctg aag tgc ttc gcc cgc tac ccc gac cac atg aag	240
	Phe Gly Tyr Gly Leu Lys Cys Phe Ala Arg Tyr Pro Asp His Met Lys	
	65 70 75 80	
25	cgg cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag	288
	Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu	
	85 90 95	
30	cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag	336
	Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu	
	100 105 110	
35	gtg aag ttc gag ggc	351
	Val Lys Phe Glu Gly	
	115	
35	YFP F1C, Q69K mutation and pos. 1 Met removed	
	SEQ ID NOS:368 & 369	
40	gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc	48
	Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val	
	1 5 10 15	
45	gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag	96
	Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu	
	20 25 30	
50	ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc tgc	144
	Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys	
	35 40 45	
55	acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ttc	192
	Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe	
	50 55 60	
55	ggc tac ggc ctg aag tgc ttc gcc cgc tac ccc gac cac atg aag cgg	240
	Gly Tyr Gly Leu Lys Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg	
	65 70 75 80	

	cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc	288
	His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg	
	85 90 95	
5	acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag gtg	336
	Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val	
	100 105 110	
10	aag ttc gag ggc	348
	Lys Phe Glu Gly	
	115	
15	citrine F1C, V68L, Q69M mutations	
	SEQ ID NOS:370 & 371	
20	atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg	48
	Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu	
	1 5 10 15	
25	gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc	96
	Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly	
	20 25 30	
30	gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc	144
	Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile	
	35 40 45	
35	tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc	192
	Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr	
	50 55 60	
40	ttc ggc tac ggc ctg atg tgc ttc gcc cgc tac ccc gac cac atg aag	240
	Phe Gly Tyr Gly Leu Met Cys Phe Ala Arg Tyr Pro Asp His Met Lys	
	65 70 75 80	
45	cgg cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag	288
	Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu	
	85 90 95	
50	cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag	336
	Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu	
	100 105 110	
55	gtg aag ttc gag ggc	351
	Val Lys Phe Glu Gly	
	115	
50	citrine F1C, V68L, Q69M mutations and pos. 1 Met removed	
	SEQ ID NOS:372 & 373	
55	gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc	48
	Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val	
	1 5 10 15	

	gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu	96
	20 25 30	
5	ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc tgc Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys	144
	35 40 45	
10	acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ttc Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe	192
	50 55 60	
15	ggc tac ggc ctg atg tgc ttc gcc cgc tac ccc gac cac atg aag cgg Gly Tyr Gly Leu Met Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg	240
	65 70 75 80	
20	cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg	288
	85 90 95	
	acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag gtg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val	336
	100 105 110	
25	aag ttc gag ggc Lys Phe Glu Gly	348
	115	
30	YFP F1C, F46L, F64L mutations SEQ ID NOS:374 & 375	
35	atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu	48
	1 5 10 15	
40	gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly	96
	20 25 30	
45	gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ctg atc Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Leu Ile	144
	35 40 45	
50	tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr	192
	50 55 60	
	ctg ggc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag Leu Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys	240
	65 70 75 80	
55	cgg cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu	288
	85 90 95	



	cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag	336
	Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu	
	100 105 110	
5	gtg aag ttc gag ggc	351
	Val Lys Phe Glu Gly	
	115	
10	YFP F1C, F46L, F64L mutations and pos. 1 Met removed	
	SEQ ID NOS:376 & 377	
15	gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc	48
	Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val	
	1 5 10 15	
20	gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag	96
	Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu	
	20 25 30	
25	ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ctg atc tgc	144
	Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Leu Ile Cys	
	35 40 45	
30	acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ctg	192
	Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Leu	
	50 55 60	
35	ggc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag cgg	240
	Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg	
	65 70 75 80	
40	cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc	288
	His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg	
	85 90 95	
45	acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag gtg	336
	Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val	
	100 105 110	
50	aag ttc gag ggc	348
	Lys Phe Glu Gly	
	115	
55	CFP F1C, F64L mutation	
	SEQ ID NOS:378 & 379	
50	atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg	48
	Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu	
	1 5 10 15	
55	gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc	96
	Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly	
	20 25 30	

	gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc	144
	Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile	
	35 40 45	
5	tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc	192
	Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr	
	50 55 60	
10	ctc ggc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag	240
	Leu Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys	
	65 70 75 80	
15	cgg cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag	288
	Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu	
	85 90 95	
20	cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag	336
	Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu	
	100 105 110	
25	gtg aag ttc gag ggc	351
	Val Lys Phe Glu Gly	
	115	
	CFP F1C, F64L mutation and pos. 1 Met removed	
	SEQ ID NOS:380 & 381	
30	gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc	48
	Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val	
	1 5 10 15	
35	gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag	96
	Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu	
	20 25 30	
40	ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc tgc	144
	Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys	
	35 40 45	
45	acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ctc	192
	Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Leu	
	50 55 60	
50	ggc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag cgg	240
	Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg	
	65 70 75 80	
55	cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc	288
	His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg	
	85 90 95	
55	acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag gtg	336
	Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val	
	100 105 110	

	aag ttc gag ggc	348
	Lys Phe Glu Gly	
	115	
5	CFP F1C, Y66W mutation	
	SEQ ID NOS:382 & 383	
10	atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg	48
	Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu	
	1 5 10 15	
15	gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc	96
	Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly	
	20 25 30	
20	gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc	144
	Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile	
	35 40 45	
25	tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc	192
	Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr	
	50 55 60	
30	ttc ggc tgg ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag	240
	Phe Gly Trp Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys	
	65 70 75 80	
35	cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag	336
	Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu	
	100 105 110	
40	gtg aag ttc gag ggc	351
	Val Lys Phe Glu Gly	
	115	
45	CFP F1C, Y66W mutation and pos. 1 Met removed	
	SEQ ID NOS:384 & 385	
50	gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc	48
	Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val	
	1 5 10 15	
55	gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag	96
	Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu	
	20 25 30	
55	ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc tgc	144
	Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys	
	35 40 45	

	acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ttc	192
	Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe	
	50 55 60	
5	ggc tgg ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag cgg	240
	Gly Trp Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg	
	65 70 75 80	
10	cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc	288
	His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg	
	85 90 95	
15	acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag gtg	336
	Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val	
	100 105 110	
	aag ttc gag ggc	348
	Lys Phe Glu Gly	
	115	
20		
	CFP FlC, S65A mutation	
	SEQ ID NOS:386 & 387	
25	atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg	48
	Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu	
	1 5 10 15	
30	gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc	96
	Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly	
	20 25 30	
35	gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc	144
	Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile	
	35 40 45	
	tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc	192
	Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr	
	50 55 60	
40		
	ttc gcc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag	240
	Phe Ala Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys	
	65 70 75 80	
45	cgg cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag	288
	Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu	
	85 90 95	
50	cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag	336
	Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu	
	100 105 110	
	gtg aag ttc gag ggc	351
	Val Lys Phe Glu Gly	
55	115	

CFP F1C, S65A mutation and pos. 1 Met removed  
SEQ ID NOS:388 & 389

5	gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val 1 5 10 15	48
10	gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu 20 25 30	96
15	ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc tgc Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys 35 40 45	144
	acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ttc Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe 50 55 60	192
20	gcc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag cgg Ala Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg 65 70 75 80	240
25	cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg 85 90 95	288
30	acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag gtg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val 100 105 110	336
35	aag ttc gag ggc Lys Phe Glu Gly 115	348

CFP F1C, S65A,Y66W,and S72A mutations  
SEQ ID NOS:390 & 391

40	atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu 1 5 10 15	48
45	gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly 20 25 30	96
50	gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile 35 40 45	144
55	tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr 50 55 60	192

	ttc gcc tgg ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag	240
	Phe Ala Trp Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys	
	65 70 75 80	
5	cgg cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag	288
	Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu	
	85 90 95	
10	cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag	336
	Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu	
	100 105 110	
15	gtg aag ttc gag ggc	351
	Val Lys Phe Glu Gly	
	115	
20	CFP F1C, S65A, Y66W, S72A mutations and pos. 1 Met removed SEQ ID NOS:392 & 393	
25	gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc	48
	Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val	
	1 5 10 15	
30	gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag	96
	Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu	
	20 25 30	
35	ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc tgc	144
	Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys	
	35 40 45	
40	acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ttc	192
	Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe	
	50 55 60	
45	gcc tgg ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag cgg	240
	Ala Trp Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg	
	65 70 75 80	
50	cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc	288
	His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg	
	85 90 95	
55	acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag gtg	336
	Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val	
	100 105 110	
60	aag ttc gag ggc	348
	Lys Phe Glu Gly	
	115	

CFP F1C, F64L,S65T,Y66W mutations  
SEQ ID NOS:394 & 395

5	atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu	48
	1 5 10 15	
10	gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly	96
	20 25 30	
15	gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile	144
	35 40 45	
20	tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr	192
	50 55 60	
25	ctg acc tgg ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag Leu Thr Trp Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys	240
	65 70 75 80	
30	cgg cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu	288
	85 90 95	
35	cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu	336
	100 105 110	
40	gtg aag ttc gag ggc Val Lys Phe Glu Gly	351
	115	

CFP F1C, F64L,S65T,Y66W mutations and pos. 1 Met removed  
SEQ ID NOS:396 & 397

45	gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val	48
	1 5 10 15	
50	gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu	96
	20 25 30	
55	ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc tgc Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys	144
	35 40 45	
60	acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ctg Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Leu	192
	50 55 60	

	acc tgg ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag cgg	240
	Thr Trp Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg	
	65 70 75 80	
5	cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc	288
	His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg	
	85 90 95	
10	acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag gtg	336
	Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val	
	100 105 110	
15	aag ttc gag ggc	348
	Lys Phe Glu Gly	
	115	
20	BFP F1C, Y66H mutation	
	SEQ ID NOS:398 & 399	
25	atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg	48
	Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu	
	1 5 10 15	
30	gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc	96
	Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly	
	20 25 30	
35	gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc	144
	Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile	
	35 40 45	
40	tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc	192
	Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr	
	50 55 60	
45	ttc ggc cac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg cgc	240
	Phe Gly His Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Arg	
	65 70 75 80	
50	cgg cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag	288
	Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu	
	85 90 95	
55	cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag	336
	Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu	
	100 105 110	
60	gtg aag ttc gag ggc	351
	Val Lys Phe Glu Gly	
	115	
65		



BFP F1C, Y66H mutation and pos. 1 Met removed  
SEQ ID NOS:400 & 401

5	gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val	48
	1 5 10 15	
10	gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu	96
	20 25 30	
15	ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc tgc Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys	144
	35 40 45	
	acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ttc Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe	192
	50 55 60	
20	ggc cac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg cgc cgg Gly His Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Arg Arg	240
	65 70 75 80	
25	cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg	288
	85 90 95	
30	acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag gtg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val	336
	100 105 110	
35	aag ttc gag ggc Lys Phe Glu Gly	348
	115	

40 BFP F1C, F64L,Y66H mutations  
SEQ ID NOS:402 & 403

45	atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu	48
	1 5 10 15	
	gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly	96
	20 25 30	
50	gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile	144
	35 40 45	
55	tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr	192
	50 55 60	

	ctc ggc cac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg cgc	240
	Leu Gly His Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Arg	
	65 70 75 80	
5	cgg cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag	288
	Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu	
	85 90 95	
10	cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag	336
	Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu	
	100 105 110	
	gtg aag ttc gag ggc	351
15	Val Lys Phe Glu Gly	
	115	
20	BFP F1C, F64L,Y66H mutations and pos. 1 Met removed	
	SEQ ID NOS:404 & 405	
	gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc	48
25	Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val	
	1 5 10 15	
	gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag	96
	Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu	
	20 25 30	
30	ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc tgc	144
	Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys	
	35 40 45	
35	acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ctc	192
	Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Leu	
	50 55 60	
	ggc cac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg cgc cgg	240
40	Gly His Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Arg Arg	
	65 70 75 80	
	cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc	288
45	His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg	
	85 90 95	
	acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag gtg	336
	Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val	
	100 105 110	
50	aag ttc gag ggc	348
	Lys Phe Glu Gly	
	115	
55		

YFP F2C, with Met added @ pos. 1  
(YFP F2C corresponds to aa residues 118-239 of YFP)  
SEQ ID NOS:406 & 407

5	atg gac acc ctg gtg aac cgc atc gag ctg aag ggc atc gac ttc aag	48
	Met Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys	
	1 5 10 15	
10	gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac tac aac agc	96
	Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser	
	20 25 30	
15	cac aac gtc tat atc atg gcc gac aag cag aag aac ggc atc aag gtg	144
	His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val	
	35 40 45	
20	aac ttc aag atc cgc cac aac atc gag gac ggc agc gtg cag ctc gcc	192
	Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala	
	50 55 60	
25	gac cac tac cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg	240
	Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu	
	65 70 75 80	
30	ccc gac aac cac tac ctg agc tac cag tcc gcc ctg agc aaa gac ccc	288
	Pro Asp Asn His Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro	
	85 90 95	
35	aac gag aag cgc gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc	336
	Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala	
	100 105 110	
40	ggg atc act ctc ggc atg gac gag ctg tac aag	369
	Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys	
	115 120	

YFP F2C, Y203F mutation  
SEQ ID NOS:408 & 409

40	gac acc ctg gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag	48
	Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu	
	1 5 10 15	
45	gac ggc aac atc ctg ggg cac aag ctg gag tac aac tac aac agc cac	96
	Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His	
	20 25 30	
50	aac gtc tat atc atg gcc gac aag cag aag aac ggc atc aag gtg aac	144
	Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn	
	35 40 45	
55	ttc aag atc cgc cac aac atc gag gac ggc agc gtg cag ctc gcc gac	192
	Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp	
	50 55 60	

	cac tac cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc	240
	His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro	
	65 70 75 80	
5	gac aac cac tac ctg agc ttc cag tcc gcc ctg agc aaa gac ccc aac	288
	Asp Asn His Tyr Leu Ser Phe Gln Ser Ala Leu Ser Lys Asp Pro Asn	
	85 90 95	
10	gag aag cgc gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg	336
	Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly	
	100 105 110	
15	atc act ctc ggc atg gac gag ctg tac aag	366
	Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys	
	115 120	
20	YFP F2C, Y203F mutation and Met added @ pos. 1 SEQ ID NOS:410 & 411	
25	atg gac acc ctg gtg aac cgc atc gag ctg aag ggc atc gac ttc aag	48
	Met Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys	
	1 5 10 15	
30	gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac tac aac agc	96
	Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser	
	20 25 30	
35	cac aac gtc tat atc atg gcc gac aag cag aag aac ggc atc aag gtg	144
	His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val	
	35 40 45	
40	aac ttc aag atc cgc cac aac atc gag gac ggc agc gtg cag ctc gcc	192
	Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala	
	50 55 60	
45	gac cac tac cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg	240
	Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu	
	65 70 75 80	
50	ccc gac aac cac tac ctg agc ttc cag tcc gcc ctg agc aaa gac ccc	288
	Pro Asp Asn His Tyr Leu Ser Phe Gln Ser Ala Leu Ser Lys Asp Pro	
	85 90 95	
55	aac gag aag cgc gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc	336
	Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala	
	100 105 110	
60	ggg atc act ctc ggc atg gac gag ctg tac aag	369
	Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys	
	115 120	

YFP F2C, Y203H mutation  
SEQ ID NOS:412 & 413

5	gac acc ctg gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu 1 5 10 15	48
10	gac ggc aac atc ctg ggg cac aag ctg gag tac aac tac aac agc cac Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His 20 25 30	96
15	aac gtc tat atc atg gcc gac aag cag aag aac ggc atc aag gtg aac Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn 35 40 45	144
20	ttc aag atc cgc cac aac atc gag gac ggc agc gtg cag ctc gcc gac Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp 50 55 60	192
25	cac tac cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro 65 70 75 80	240
30	gac aac cac tac ctg agc cac cag tcc gcc ctg agc aaa gac ccc aac Asp Asn His Tyr Leu Ser His Gln Ser Ala Leu Ser Lys Asp Pro Asn 85 90 95	288
35	gag aag cgc gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly 100 105 110	336
40	atc act ctc ggc atg gac gag ctg tac aag Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys 115 120	366

YFP F2C, Y203H mutation and Met added @ pos. 1  
SEQ ID NOS:414 & 415

45	atg gac acc ctg gtg aac cgc atc gag ctg aag ggc atc gac ttc aag Met Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys 1 5 10 15	48
50	gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac tac aac agc Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser 20 25 30	96
55	cac aac gtc tat atc atg gcc gac aag cag aag aac ggc atc aag gtg His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val 35 40 45	144
60	aac ttc aag atc cgc cac aac atc gag gac ggc agc gtg cag ctc gcc Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala 50 55 60	192

	gac cac tac cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg	240
	Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu	
	65 70 75 80	
5	ccc gac aac cac tac ctg agc cac cag tcc gcc ctg agc aaa gac ccc	288
	Pro Asp Asn His Tyr Leu Ser His Gln Ser Ala Leu Ser Lys Asp Pro	
	85 90 95	
10	aac gag aag cgc gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc	336
	Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala	
	100 105 110	
15	ggg atc act ctc ggc atg gac gag ctg tac aag	369
	Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys	
	115 120	
20	CFP F2C, N146I mutation (CFP F2C corresponds to aa residues 118-239 of YFP) SEQ ID NOS:416 & 417	
25	gac acc ctg gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag	48
	Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu	
	1 5 10 15	
30	gac ggc aac atc ctg ggc cac aag ctg gag tac aac tac atc agc cac	96
	Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Ile Ser His	
	20 25 30	
35	aac gtc tat atc atg gcc gac aag cag aag aac ggc atc aag gtg aac	144
	Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn	
	35 40 45	
40	ttc aag atc cgc cac aac atc gag gac ggc agc gtg cag ctc gcc gac	192
	Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp	
	50 55 60	
45	cac tac cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc	240
	His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro	
	65 70 75 80	
50	gac aac cac tac ctg agc acc cag tcc gcc ctg agc aaa gac ccc aac	288
	Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro Asn	
	85 90 95	
55	gag aag cgc gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggc	336
	Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly	
	100 105 110	
60	atc act ctc ggc atg gac gag ctg tac aag	366
	Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys	
	115 120	

CFP F2C, N146I mutation and Met added @ pos. 1  
SEQ ID NOS:418 & 419

5	atg gac acc ctg gtg aac cgc atc gag ctg aag ggc atc gac ttc aag Met Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys 1 5 10 15	48
10	gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac tac atc agc Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Ile Ser 20 25 30	96
15	cac aac gtc tat atc atg gcc gac aag cag aag aac ggc atc aag gtg His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val 35 40 45	144
20	aac ttc aag atc cgc cac aac atc gag gac ggc agc gtg cag ctc gcc Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala 50 55 60	192
25	gac cac tac cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu 65 70 75 80	240
30	ccc gac aac cac tac ctg agc acc cag tcc gcc ctg agc aaa gac ccc Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro 85 90 95	288
35	aac gag aag cgc gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala 100 105 110	336
40	ggg atc act ctc ggc atg gac gag ctg tac aag Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys 115 120	369

CFP F2C, M153T mutation  
SEQ ID NOS:420 & 421

45	gac acc ctg gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu 1 5 10 15	48
50	gac ggc aac atc ctg ggg cac aag ctg gag tac aac tac aac agc cac Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His 20 25 30	96
55	aac gtc tat atc acc gcc gac aag cag aag aac ggc atc aag gtg aac Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn 35 40 45	144
60	ttc aag atc cgc cac aac atc gag gac ggc agc gtg cag ctc gcc gac Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp 50 55 60	192

	cac tac cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc	240
	His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro	
	65 70 75 80	
5	gac aac cac tac ctg agc acc cag tcc gcc ctg agc aaa gac ccc aac	288
	Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro Asn	
	85 90 95	
10	gag aag cgc gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg	336
	Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly	
	100 105 110	
15	atc act ctc ggc atg gac gag ctg tac aag	366
	Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys	
	115 120	
20	CFP F2C, M153T mutation and Met added @ pos. 1 SEQ ID NOS:422 & 423	
25	atg gac acc ctg gtg aac cgc atc gag ctg aag ggc atc gac ttc aag	48
	Met Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys	
	1 5 10 15	
30	gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac tac aac agc	96
	Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser	
	20 25 30	
35	cac aac gtc tat atc acc gcc gac aag cag aag aac ggc atc aag gtg	144
	His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly Ile Lys Val	
	35 40 45	
40	aac ttc aag atc cgc cac aac atc gag gac ggc agc gtg cag ctc gcc	192
	Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala	
	50 55 60	
45	gac cac tac cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg	240
	Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu	
	65 70 75 80	
50	ccc gac aac cac tac ctg agc acc cag tcc gcc ctg agc aaa gac ccc	288
	Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro	
	85 90 95	
55	aac gag aag cgc gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc	336
	Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala	
	100 105 110	
60	ggg atc act ctc ggc atg gac gag ctg tac aag	369
	Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys	
	115 120	



CFP F2C, N146I,M153T mutations  
SEQ ID NOS:424 & 425

5	gac acc ctg gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu 1 5 10 15	48
10	gac ggc aac atc ctg ggg cac aag ctg gag tac aac tac atc agc cac Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Ile Ser His 20 25 30	96
15	aac gtc tat atc acc gcc gac aag cag aag aac ggc atc aag gtg aac Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn 35 40 45	144
	ttc aag atc cgc cac aac atc gag gac ggc agc gtg cag ctc gcc gac Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp 50 55 60	192
20	cac tac cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro 65 70 75 80	240
25	gac aac cac tac ctg agc acc cag tcc gcc ctg agc aaa gac ccc aac Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro Asn 85 90 95	288
30	gag aag cgc gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly 100 105 110	336
35	atc act ctc ggc atg gac gag ctg tac aag Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys 115 120	366

CFP F2C, N146I, M153T mutations and Met added @ pos. 1  
SEQ ID NOS:426 & 427

40	atg gac acc ctg gtg aac cgc atc gag ctg aag ggc atc gac ttc aag Met Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys 1 5 10 15	48
45	gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac tac atc agc Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Ile Ser 20 25 30	96
50	cac aac gtc tat atc acc gcc gac aag cag aag aac ggc atc aag gtg His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly Ile Lys Val 35 40 45	144
55	aac ttc aag atc cgc cac aac atc gag gac ggc agc gtg cag ctc gcc Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala 50 55 60	192

	gac cac tac cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg	240
	Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu	
	65 70 75 80	
5	ccc gac aac cac tac ctg agc acc cag tcc gcc ctg agc aaa gac ccc	288
	Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro	
	85 90 95	
10	aac gag aag cgc gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc	336
	Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala	
	100 105 110	
15	ggg atc act ctc ggc atg gac gag ctg tac aag	369
	Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys	
	115 120	
20	CFP F2C, V163A mutation SEQ ID NOS:428 & 429	
25	gac acc ctg gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag	48
	Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu	
	1 5 10 15	
30	gac ggc aac atc ctg ggc cac aag ctg gag tac aac tac aac agc cac	96
	Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His	
	20 25 30	
35	aac gtc tat atc atg gcc gac aag cag aag aac ggc atc aag gcc aac	144
	Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Ala Asn	
	35 40 45	
40	ttc aag atc cgc cac aac atc gag gac ggc agc gtg cag ctc gcc gac	192
	Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp	
	50 55 60	
45	cac tac cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc	240
	His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro	
	65 70 75 80	
50	gac aac cac tac ctg agc acc cag tcc gcc ctg agc aaa gac ccc aac	288
	Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro Asn	
	85 90 95	
55	gag aag cgc gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg	336
	Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly	
	100 105 110	
60	atc act ctc ggc atg gac gag ctg tac aag	366
	Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys	
	115 120	

CFP F2C, V163A mutation and Met added @ pos. 1  
SEQ ID NOS:430 & 431

5	atg gac acc ctg gtg aac cgc atc gag ctg aag ggc atc gac ttc aag Met Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys 1 5 10 15	48
10	gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac tac aac agc Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser 20 25 30	96
15	cac aac gtc tat atc atg gcc gac aag cag aag aac ggc atc aag gcc His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Ala 35 40 45	144
20	aac ttc aag atc cgc cac aac atc gag gac ggc agc gtg cag ctc gcc Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala 50 55 60	192
25	gac cac tac cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu 65 70 75 80	240
30	ccc gac aac cac tac ctg agc acc cag tcc gcc ctg agc aaa gac ccc Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro 85 90 95	288
35	aac gag aag cgc gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala 100 105 110	336
40	ggg atc act ctc ggc atg gac gag ctg tac aag Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys 115 120	369

CFP F2C, N146I,V163A mutations  
SEQ ID NOS:432 & 433

45	gac acc ctg gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu 1 5 10 15	48
50	gac ggc aac atc ctg ggg cac aag ctg gag tac aac tac atc agc cac Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Ile Ser His 20 25 30	96
55	aac gtc tat atc atg gcc gac aag cag aag aac ggc atc aag gcc aac Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Ala Asn 35 40 45	144
60	ttc aag atc cgc cac aac atc gag gac ggc agc gtg cag ctc gcc gac Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp 50 55 60	192

	cac tac cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc	240
	His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro	
	65 70 75 80	
5	gac aac cac tac ctg agc acc cag tcc gcc ctg agc aaa gac ccc aac	288
	Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro Asn	
	85 90 95	
10	gag aag cgc gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg	336
	Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly	
	100 105 110	
15	atc act ctc ggc atg gac gag ctg tac aag	366
	Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys	
	115 120	
20	CFP F2C, N146I,V163A mutations and Met added @ pos. 1 SEQ ID NOS:434 & 435	
25	atg gac acc ctg gtg aac cgc atc gag ctg aag ggc atc gac ttc aag	48
	Met Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys	
	1 5 10 15	
30	gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac tac atc agc	96
	Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Ile Ser	
	20 25 30	
35	cac aac gtc tat atc atg gcc gac aag cag aag aac ggc atc aag gcc	144
	His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Ala	
	35 40 45	
40	aac ttc aag atc cgc cac aac atc gag gac ggc agc gtg cag ctc gcc	192
	Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala	
	50 55 60	
45	gac cac tac cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg	240
	Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu	
	65 70 75 80	
50	ccc gac aac cac tac ctg agc acc cag tcc gcc ctg agc aaa gac ccc	288
	Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro	
	85 90 95	
55	aac gag aag cgc gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc	336
	Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala	
	100 105 110	
60	ggg atc act ctc ggc atg gac gag ctg tac aag	369
	Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys	
	115 120	

CFP F2C, M153T, V163A mutations  
SEQ ID NOS:436 & 437

5	gac acc ctg gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu 1 5 10 15	48
10	gac ggc aac atc ctg ggg cac aag ctg gag tac aac tac aac agc cac Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His 20 25 30	96
15	aac gtc tat atc acc gcc gac aag cag aag aac ggc atc aag gcc aac Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly Ile Lys Ala Asn 35 40 45	144
20	ttc aag atc cgc cac aac atc gag gac ggc agc gtg cag ctc gcc gac Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp 50 55 60	192
25	cac tac cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro 65 70 75 80	240
30	gac aac cac tac ctg agc acc cag tcc gcc ctg agc aaa gac ccc aac Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro Asn 85 90 95	288
35	gag aag cgc gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly 100 105 110	336
40	atc act ctc ggc atg gac gag ctg tac aag Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys 115 120	366

CFP F2C, M153T, V163A mutations and Met added @ pos. 1  
SEQ ID NOS:438 & 439

45	atg gac acc ctg gtg aac cgc atc gag ctg aag ggc atc gac ttc aag Met Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys 1 5 10 15	48
50	gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac tac aac agc Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser 20 25 30	96
55	cac aac gtc tat atc acc gcc gac aag cag aag aac ggc atc aag gcc His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly Ile Lys Ala 35 40 45	144
60	aac ttc aag atc cgc cac aac atc gag gac ggc agc gtg cag ctc gcc Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala 50 55 60	192

	gac cac tac cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg	240
	Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu	
	65 70 75 80	
5	ccc gac aac cac tac ctg agc acc cag tcc gcc ctg agc aaa gac ccc	288
	Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro	
	85 90 95	
10	aac gag aag cgc gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc	336
	Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala	
	100 105 110	
15	ggg atc act ctc ggc atg gac gag ctg tac aag	369
	Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys	
	115 120	
20	CFP F2C, N146I,M153T,and V163A mutations SEQ ID NOS:440 & 441	
25	gac acc ctg gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag	48
	Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu	
	1 5 10 15	
30	gac ggc aac atc ctg ggc cac aag ctg gag tac aac tac atc agc cac	96
	Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Ile Ser His	
	20 25 30	
35	aac gtc tat atc acc gcc gac aag cag aag aac ggc atc aag gcc aac	144
	Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly Ile Lys Ala Asn	
	35 40 45	
40	ttc aag atc cgc cac aac atc gag gac ggc agc gtg cag ctc gcc gac	192
	Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp	
	50 55 60	
45	cac tac cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc	240
	His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro	
	65 70 75 80	
50	gac aac cac tac ctg agc acc cag tcc gcc ctg agc aaa gac ccc aac	288
	Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro Asn	
	85 90 95	
55	gag aag cgc gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg	336
	Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly	
	100 105 110	
60	atc act ctc ggc atg gac gag ctg tac aag	366
	Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys	
	115 120	

CFP F2C, N146I, M153T, and V163A mutations and Met added @ pos. 1  
SEQ ID NOS:442 & 443

5	atg gac acc ctg gtg aac cgc atc gag ctg aag ggc atc gac ttc aag Met Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys	48
	1 5 10 15	
10	gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac tac atc agc Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Ile Ser	96
	20 25 30	
15	cac aac gtc tat atc acc gcc gac aag cag aag aac ggc atc aag gcc His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly Ile Lys Ala	144
	35 40 45	
20	aac ttc aag atc cgc cac aac atc gag gac ggc agc gtg cag ctc gcc Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala	192
	50 55 60	
25	gac cac tac cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu	240
	65 70 75 80	
30	ccc gac aac cac tac ctg agc acc cag tcc gcc ctg agc aaa gac ccc Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro	288
	85 90 95	
35	aac gag aag cgc gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala	336
	100 105 110	
40	ggg atc act ctc ggc atg gac gag ctg tac aag Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys	369
	115 120	

CGFP F2C, M153T,T203Y mutations  
(CGFP F2C corresponds to residues 118-239 of YFP)  
SEQ ID NOS:444 & 445

45	gac acc ctg gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu	48
	1 5 10 15	
50	gac ggc aac atc ctg ggg cac aag ctg gag tac aac tac aac agc cac Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His	96
	20 25 30	
55	aac gtc tat atc acc gcc gac aag cag aag aac ggc atc aag gtg aac Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn	144
	35 40 45	
60	ttc aag atc cgc cac aac atc gag gac ggc agc gtg cag ctc gcc gac Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp	192
	50 55 60	

Position	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20
	cac	tac	cag	cag	aac	acc	ccc	atc	ggc	gac	ggc	ccc	gtg	ctg	ctg	ccc				
	His	Tyr	Gln	Gln	Asn	Thr	Pro	Ile	Gly	Asp	Gly	Pro	Val	Leu	Leu	Pro				
	65					70					75					80				
5																				
	gac	aac	cac	tac	ctg	agc	tac	cag	tcc	gcc	ctg	agc	aaa	gac	ccc	aac				
	Asp	Asn	His	Tyr	Leu	Ser	Tyr	Gln	Ser	Ala	Leu	Ser	Lys	Asp	Pro	Asn				
					85					90					95					
10																				
	gag	aag	cgc	gat	cac	atg	gtc	ctg	ctg	gag	ttc	gtg	acc	gcc	gcc	ggg				
	Glu	Lys	Arg	Asp	His	Met	Val	Leu	Leu	Glu	Phe	Val	Thr	Ala	Ala	Gly				
				100				105					110							
	atc	act	ctc	ggc	atg	gac	gag	ctg	tac	aag										
15	Ile	Thr	Leu	Gly	Met	Asp	Glu	Leu	Tyr	Lys										
			115					120												
20																				
	CGFP F2C, M153T,T203Y mutations and Met added @ pos. 1																			
	SEQ ID NOS:446 & 447																			
	atg	gac	acc	ctg	gtg	aac	cgc	atc	gag	ctg	aag	ggc	atc	gac	ttc	aag				
25	Met	Asp	Thr	Leu	Val	Asn	Arg	Ile	Glu	Leu	Lys	Gly	Ile	Asp	Phe	Lys				
	1			5					10				15							
	gag	gac	ggc	aac	atc	ctg	ggg	cac	aag	ctg	gag	tac	aac	tac	aac	agc				
	Glu	Asp	Gly	Asn	Ile	Leu	Gly	His	Lys	Leu	Glu	Tyr	Asn	Tyr	Asn	Ser				
30				20				25					30							
	cac	aac	gtc	tat	atc	acc	gcc	gac	aag	cag	aag	aac	ggc	atc	aag	gtg				
	His	Asn	Val	Tyr	Ile	Thr	Ala	Asp	Lys	Gln	Lys	Asn	Gly	Ile	Lys	Val				
			35				40						45							
35																				
	aac	ttc	aag	atc	cgc	cac	aac	atc	gag	gac	ggc	agc	gtg	cag	ctc	gcc				
	Asn	Phe	Lys	Ile	Arg	His	Asn	Ile	Glu	Asp	Gly	Ser	Val	Gln	Leu	Ala				



CGFP F2C, V163A,T203Y mutations  
SEQ ID NOS:448 & 449

5	gac acc ctg gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu 1 5 10 15	48
10	gac ggc aac atc ctg ggg cac aag ctg gag tac aac tac aac agc cac Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His 20 25 30	96
15	aac gtc tat atc atg gcc gac aag cag aag aac ggc atc aag gcc aac Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Ala Asn 35 40 45	144
20	ttc aag atc cgc cac aac atc gag gac ggc agc gtg cag ctc gcc gac Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp 50 55 60	192
25	cac tac cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro 65 70 75 80	240
30	gac aac cac tac ctg agc tac cag tcc gcc ctg agc aaa gac ccc aac Asp Asn His Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn 85 90 95	288
35	gag aag cgc gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly 100 105 110	336
40	atc act ctc ggc atg gac gag ctg tac aag Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys 115 120	366

CGFP F2C, V163A,T203Y mutations and Met added @ pos. 1  
SEQ ID NOS:450 & 451

45	atg gac acc ctg gtg aac cgc atc gag ctg aag ggc atc gac ttc aag Met Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys 1 5 10 15	48
50	gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac tac aac agc Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser 20 25 30	96
55	cac aac gtc tat atc atg gcc gac aag cag aag aac ggc atc aag gcc His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Ala 35 40 45	144
60	aac ttc aag atc cgc cac aac atc gag gac ggc agc gtg cag ctc gcc Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala 50 55 60	192

	gac cac tac cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg	240
	Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu	
	65 70 75 80	
5	ccc gag aac cac tac ctg agc tac cag tcc gcc ctg agc aaa gag ccc	288
	Pro Asp Asn His Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro	
	85 90 95	
10	aac gag aag cgc gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc	336
	Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala	
	100 105 110	
15	ggg atc act ctg ggc atg gac gag ctg tac aag	369
	Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys	
	115 120	
20	CGFP F2C, N146I,M153T,and T203Y mutations SEQ ID NOS:452 & 453	
25	gac acc ctg gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag	48
	Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu	
	1 5 10 15	
30	gac ggc aac atc ctg ggc cac aag ctg gag tac aac tac atc agc cac	96
	Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Ile Ser His	
	20 25 30	
35	aac gtc tat atc acc gcc gac aag cag aag aac ggc atc aag gtg aac	144
	Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn	
	35 40 45	
40	ttc aag atc cgc cac aac atc gag gac ggc agc gtg cag ctg gcc gag	192
	Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp	
	50 55 60	
45	cac tac cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc	240
	His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro	
	65 70 75 80	
50	gac aac cac tac ctg agc tac cag tcc gcc ctg agc aaa gag ccc aac	288
	Asp Asn His Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn	
	85 90 95	
55	gag aag cgc gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg	336
	Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly	
	100 105 110	
60	atc act ctg ggc atg gac gag ctg tac aag	366
	Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys	
	115 120	

CGFP F2C, N146I,M153T,and T203Y mutations and Met added @ pos. 1  
SEQ ID NOS:454 & 455

5	atg gac acc ctg gtg aac cgc atc gag ctg aag ggc atc gac ttc aag Met Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys	48
	1 5 10 15	
10	gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac tac atc agc Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Ile Ser	96
	20 25 30	
15	cac aac gtc tat atc acc gcc gac aag cag aag aac ggc atc aag gtg His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly Ile Lys Val	144
	35 40 45	
20	aac ttc aag atc cgc cac aac atc gag gac ggc agc gtg cag ctc gcc Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala	192
	50 55 60	
25	gac cac tac cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu	240
	65 70 75 80	
30	ccc gac aac cac tac ctg agc tac cag tcc gcc ctg agc aaa gac ccc Pro Asp Asn His Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro	288
	85 90 95	
35	aac gag aag cgc gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala	336
	100 105 110	
40	ggg atc act ctc ggc atg gac gag ctg tac aag Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys	369
	115 120	

CGFP F2C, M153T,V163A,and T203Y mutations  
SEQ ID NOS:456 & 457

45	gac acc ctg gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu	48
	1 5 10 15	
50	gac ggc aac atc ctg ggg cac aag ctg gag tac aac tac aac agc cac Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His	96
	20 25 30	
55	aac gtc tat atc acc gcc gac aag cag aag aac ggc atc aag gcc aac Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly Ile Lys Ala Asn	144
	35 40 45	
60	ttc aag atc cgc cac aac atc gag gac ggc agc gtg cag ctc gcc gac Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp	192
	50 55 60	

	cac tac cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc	240
	His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro	
	65 70 75 80	
5	gac aac cac tac ctg agc tac cag tcc gcc ctg agc aaa gac ccc aac	288
	Asp Asn His Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn	
	85 90 95	
10	gag aag cgc gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg	336
	Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly	
	100 105 110	
15	atc act ctc ggc atg gac gag ctg tac aag	366
	Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys	
	115 120	
20	CGFP F2C, M153T,V163A,and T203Y mutations and Met added @ pos. 1 SEQ ID NOS:458 & 459	
25	atg gac acc ctg gtg aac cgc atc gag ctg aag ggc atc gac ttc aag	48
	Met Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys	
	1 5 10 15	
30	gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac tac aac agc	96
	Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser	
	20 25 30	
35	cac aac gtc tat atc acc gcc gac aag cag aag aac ggc atc aag gcc	144
	His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly Ile Lys Ala	
	35 40 45	
40	aac ttc aag atc cgc cac aac atc gag gac ggc agc gtg cag ctc gcc	192
	Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala	
	50 55 60	
45	gac cac tac cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg	240
	Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu	
	65 70 75 80	
50	ccc gac aac cac tac ctg agc tac cag tcc gcc ctg agc aaa gac ccc	288
	Pro Asp Asn His Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro	
	85 90 95	
55	aac gag aag cgc gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc	336
	Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala	
	100 105 110	
60	ggg atc act ctc ggc atg gac gag ctg tac aag	369
	Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys	
	115 120	

CGFP F2C, N146I,M153T,V163A,and T203Y mutations  
SEQ ID NOS:460 & 461

5	gac acc ctg gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu	48
	1 5 10 15	
10	gac ggc aac atc ctg ggg cac aag ctg gag tac aac tac atc agc cac Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Ile Ser His	96
	20 25 30	
15	aac gtc tat atc acc gcc gac aag cag aag aac ggc atc aag gcc aac Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly Ile Lys Ala Asn	144
	35 40 45	
	ttc aag atc cgc cac aac atc gag gac ggc agc gtg cag ctc gcc gac Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp	192
	50 55 60	
20	cac tac cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro	240
	65 70 75 80	
25	gac aac cac tac ctg agc tac cag tcc gcc ctg agc aaa gac ccc aac Asp Asn His Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn	288
	85 90 95	
30	gag aag cgc gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly	336
	100 105 110	
35	atc act ctc ggc atg gac gag ctg tac aag Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys	366
	115 120	

CGFP F2C, N146I,M153T,V163A,and T203Y mutations and Met added @ pos. 1  
SEQ ID NOS:462 & 463

40	atg gac acc ctg gtg aac cgc atc gag ctg aag ggc atc gac ttc aag Met Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys	48
	1 5 10 15	
45	gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac tac atc agc Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Ile Ser	96
	20 25 30	
50	cac aac gtc tat atc acc gcc gac aag cag aag aac ggc atc aag gcc His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly Ile Lys Ala	144
	35 40 45	
55	aac ttc aag atc cgc cac aac atc gag gac ggc agc gtg cag ctc gcc Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala	192
	50 55 60	

	gac cac tac cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg	240
	Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu	
	65 70 75 80	
5	ccc gac aac cac tac ctg agc tac cag tcc gcc ctg agc aaa gac ccc	288
	Pro Asp Asn His Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro	
	85 90 95	
10	aac gag aag cgc gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc	336
	Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala	
	100 105 110	
15	ggg atc act ctc ggc atg gac gag ctg tac aag	369
	Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys	
	115 120	
20	BFP F2C, Y145F mutation (BFP F2C corresponds to aa residues 118-239 of YFP) SEQ ID NOS:464 & 465	
25	gac acc ctg gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag	48
	Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu	
	1 5 10 15	
30	gac ggc aac atc ctg ggc cac aag ctg gag tac aac ttc aac agc cac	96
	Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Phe Asn Ser His	
	20 25 30	
35	aac gtc tat atc atg gcc gac aag cag aag aac ggc atc aag gtg aac	144
	Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn	
	35 40 45	
40	ttc aag atc cgc cac aac atc gag gac ggc agc gtg cag ctc gcc gac	192
	Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp	
	50 55 60	
45	cac tac cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc	240
	His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro	
	65 70 75 80	
50	gac aac cac tac ctg agc acc cag tcc gcc ctg agc aaa gac ccc aac	288
	Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro Asn	
	85 90 95	
55	gag aag cgc gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg	336
	Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly	
	100 105 110	
60	atc act ctc ggc atg gac gag ctg tac aag	366
	Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys	
	115 120	

BFP F2C, Y145F mutation and Met added @ pos. 1  
SEQ ID NOS:466 & 467

5	atg gac acc ctg gtg aac cgc atc gag ctg aag ggc atc gac ttc aag Met Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys	48
	1 5 10 15	
10	gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac ttc aac agc Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Phe Asn Ser	96
	20 25 30	
15	cac aac gtc tat atc atg gcc gac aag cag aag aac ggc atc aag gtg His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val	144
	35 40 45	
20	aac ttc aag atc cgc cac aac atc gag gac ggc agc gtg cag ctc gcc Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala	192
	50 55 60	
25	gac cac tac cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu	240
	65 70 75 80	
30	ccc gac aac cac tac ctg agc acc cag tcc gcc ctg agc aaa gac ccc Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro	288
	85 90 95	
35	aac gag aag cgc gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala	336
	100 105 110	
40	ggg atc act ctc ggc atg gac gag ctg tac aag Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys	369
	115 120	

Venus F2C, S175G mutation  
(Venus F2C corresponds to aa residues 118-239 of YFP)  
SEQ ID NOS:468 & 469

45	gac acc ctg gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu	48
	1 5 10 15	
50	gac ggc aac atc ctg ggg cac aag ctg gag tac aac tac aac agc cac Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His	96
	20 25 30	
55	aac gtc tat atc atg gcc gac aag cag aag aac ggc atc aag gtg aac Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn	144
	35 40 45	
60	ttc aag atc cgc cac aac atc gag gac ggc ggc gtg cag ctc gcc gac Phe Lys Ile Arg His Asn Ile Glu Asp Gly Gly Val Gln Leu Ala Asp	192
	50 55 60	

	cac tac cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc	240
	His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro	
	65 70 75 80	
5	gac aac cac tac ctg agc tac cag tcc gcc ctg agc aaa gac ccc aac	288
	Asp Asn His Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn	
	85 90 95	
10	gag aag cgc gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg	336
	Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly	
	100 105 110	
15	atc act ctc ggc atg gac gag ctg tac aag	366
	Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys	
	115 120	
20	Venus F2C, S175G mutation and Met added @ pos. 1 SEQ ID NOS:470 & 471	
25	atg gac acc ctg gtg aac cgc atc gag ctg aag ggc atc gac ttc aag	48
	Met Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys	
	1 5 10 15	
30	gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac tac aac agc	96
	Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser	
	20 25 30	
35	cac aac gtc tat atc atg gcc gac aag cag aag aac ggc atc aag gtg	144
	His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val	
	35 40 45	
40	aac ttc aag atc cgc cac aac atc gag gac ggc ggc gtg cag ctc gcc	192
	Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Gly Val Gln Leu Ala	
	50 55 60	
45	gac cac tac cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg	240
	Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu	
	65 70 75 80	
50	ccc gac aac cac tac ctg agc tac cag tcc gcc ctg agc aaa gac ccc	288
	Pro Asp Asn His Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro	
	85 90 95	
55	aac gag aag cgc gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc	336
	Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala	
	100 105 110	
60	ggg atc act ctc ggc atg gac gag ctg tac aag	369
	Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys	
	115 120	



Venus F2C, M153T, S175G mutations  
SEQ ID NOS:472 & 473

5	gac acc ctg gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu 1 5 10 15	48
10	gac ggc aac atc ctg ggg cac aag ctg gag tac aac tac aac agc cac Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His 20 25 30	96
15	aac gtc tat atc acc gcc gac aag cag aag aac ggc atc aag gtg aac Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn 35 40 45	144
20	ttc aag atc cgc cac aac atc gag gac ggc ggc gtg cag ctc gcc gac Phe Lys Ile Arg His Asn Ile Glu Asp Gly Gly Val Gln Leu Ala Asp 50 55 60	192
25	cac tac cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro 65 70 75 80	240
30	gac aac cac tac ctg agc tac cag tcc gcc ctg agc aaa gac ccc aac Asp Asn His Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn 85 90 95	288
35	gag aag cgc gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggc Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly 100 105 110	336
40	atc act ctc ggc atg gac gag ctg tac aag Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys 115 120	366
Venus F2C, M153T, S175G mutations and Met added @ pos. 1 SEQ ID NOS:474 & 475		
45	atg gac acc ctg gtg aac cgc atc gag ctg aag ggc atc gac ttc aag Met Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys 1 5 10 15	48
50	gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac tac aac agc Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser 20 25 30	96
55	cac aac gtc tat atc acc gcc gac aag cag aag aac ggc atc aag gtg His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly Ile Lys Val 35 40 45	144
60	aac ttc aag atc cgc cac aac atc gag gac ggc ggc gtg cag ctc gcc Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Gly Val Gln Leu Ala 50 55 60	192
65	gac cac tac cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu 65 70 75 80	240

	ccc gac aac cac tac ctg agc tac cag tcc gcc ctg agc aaa gac ccc	288
	Pro Asp Asn His Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro	
	85 90 95	
5	aac gag aag cgc gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc	336
	Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala	
	100 105 110	
10	ggg atc act ctc ggc atg gac gag ctg tac aag	369
	Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys	
	115 120	
15	Venus F2C, V163A, S175G mutations	
	SEQ ID NOS:476 & 477	
	gac acc ctg gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag	48
	Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu	
20	1 5 10 15	
	gac ggc aac atc ctg ggc cac aag ctg gag tac aac tac aac agc cac	96
	Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His	
	20 25 30	
25	aac gtc tat atc atg gcc gac aag cag aag aac ggc atc aag gcc aac	144
	Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Ala Asn	
	35 40 45	
30	ttc aag atc cgc cac aac atc gag gac ggc ggc gtg cag ctc gcc gac	192
	Phe Lys Ile Arg His Asn Ile Glu Asp Gly Gly Val Gln Leu Ala Asp	
	50 55 60	
	cac tac cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc	240
35	His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro	
	65 70 75 80	
	gac aac cac tac ctg agc tac cag tcc gcc ctg agc aaa gac ccc aac	288
	Asp Asn His Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn	
40	85 90 95	
	gag aag cgc gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg	336
	Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly	
	100 105 110	
45	atc act ctc ggc atg gac gag ctg tac aag	366
	Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys	
	115 120	
50	Venus F2C, V163A, S175G mutations and Met added @ pos. 1	
	SEQ ID NOS:478 & 479	
	atg gac acc ctg gtg aac cgc atc gag ctg aag ggc atc gac ttc aag	48
55	Met Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys	
	1 5 10 15	

	gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac tac aac agc	96
	Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser	
	20 25 30	
5	cac aac gtc tat atc atg gcc gac aag cag aag aac ggc atc aag gcc	144
	His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Ala	
	35 40 45	
10	aac ttc aag atc cgc cac aac atc gag gac ggc ggc gtg cag ctc gcc	192
	Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Gly Val Gln Leu Ala	
	50 55 60	
15	gac cac tac cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg	240
	Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu	
	65 70 75 80	
20	ccc gac aac cac tac ctg agc tac cag tcc gcc ctg agc aaa gac ccc	288
	Pro Asp Asn His Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro	
	85 90 95	
25	aac gag aag cgc gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc	336
	Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala	
	100 105 110	
30	ggg atc act ctc ggc atg gac gag ctg tac aag	369
	Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys	
	115 120	
30	Venus F2C, M153T,V163A,and S175G mutations	
	SEQ ID NOS:480 & 481	
35	gac acc ctg gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag	48
	Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu	
	1 5 10 15	
40	gac ggc aac atc ctg ggg cac aag ctg gag tac aac tac aac agc cac	96
	Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His	
	20 25 30	
45	aac gtc tat atc acc gcc gac aag cag aag aac ggc atc aag gcc aac	144
	Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly Ile Lys Ala Asn	
	35 40 45	
50	ttc aag atc cgc cac aac atc gag gac ggc ggc gtg cag ctc gcc gac	192
	Phe Lys Ile Arg His Asn Ile Glu Asp Gly Gly Val Gln Leu Ala Asp	
	50 55 60	
55	cac tac cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc	240
	His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro	
	65 70 75 80	
55	gac aac cac tac ctg agc tac cag tcc gcc ctg agc aaa gac ccc aac	288
	Asp Asn His Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn	
	85 90 95	

	gag aag cgc gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg	336
	Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly	
	100 105 110	
5	atc act ctc ggc atg gac gag ctg tac aag	366
	Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys	
	115 120	
10	Venus F2C, M153T, V163A, and S175G mutations and Met added @ pos. 1 SEQ ID NOS:482 & 483	
15	atg gac acc ctg gtg aac cgc atc gag ctg aag ggc atc gac ttc aag	48
	Met Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys	
	1 5 10 15	
20	gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac tac aac agc	96
	Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser	
	20 25 30	
25	cac aac gtc tat atc acc gcc gac aag cag aag aac ggc atc aag gcc	144
	His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly Ile Lys Ala	
	35 40 45	
30	aac ttc aag atc cgc cac aac atc gag gac ggc ggc gtg cag ctc gcc	192
	Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Gly Val Gln Leu Ala	
	50 55 60	
35	gac cac tac cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg	240
	Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu	
	65 70 75 80	
40	ccc gac aac cac tac ctg agc tac cag tcc gcc ctg agc aaa gac ccc	288
	Pro Asp Asn His Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro	
	85 90 95	
45	aac gag aag cgc gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc	336
	Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala	
	100 105 110	
50	ggg atc act ctc ggc atg gac gag ctg tac aag	369
	Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys	
	115 120	
55	YFP F1DX, position 1 Met removed (YFP F1DX fragment corresponds to aa residues 1-158 of YFP) SEQ ID NOS:484 & 485	
50	gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc	48
	Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val	
	1 5 10 15	
55	gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag	96
	Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu	
	20 25 30	

	ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc tgc	144
	Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys	
	35 40 45	
5	acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ttc	192
	Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe	
	50 55 60	
10	ggc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag cgg	240
	Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg	
	65 70 75 80	
15	cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc	288
	His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg	
	85 90 95	
20	acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag gtg	336
	Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val	
	100 105 110	
	aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc atc	384
	Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile	
	115 120 125	
25	gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac	432
	Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn	
	130 135 140	
30	tac aac agc cac aac gtc tat atc atg gcc gac aag cag	471
	Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln	
	145 150 155	
35	YFP F1DX, K79R mutation	
	SEQ ID NOS:486 & 487	
40	atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg	48
	Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu	
	1 5 10 15	
45	gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc	96
	Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly	
	20 25 30	
	gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc	144
	Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile	
	35 40 45	
50	tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc	192
	Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr	
	50 55 60	
55	ttc ggc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag	240
	Phe Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys	
	65 70 75 80	

	cgg cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag	288
	Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu	
	85 90 95	
5	cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag	336
	Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu	
	100 105 110	
10	gtg aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc	384
	Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly	
	115 120 125	
15	atc gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac	432
	Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr	
	130 135 140	
20	aac tac aac agc cac aac gtc tat atc atg gcc gac aag cag	474
	Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln	
	145 150 155	
YFP F1DX, K79R mutation, pos. 1 Met removed		
SEQ ID NOS:488 & 489		
25	gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc	48
	Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val	
	1 5 10 15	
30	gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag	96
	Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu	
	20 25 30	
35	ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc tgc	144
	Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys	
	35 40 45	
40	acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ttc	192
	Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe	
	50 55 60	
45	ggc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag cgg	240
	Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg	
	65 70 75 80	
50	cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc	288
	His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg	
	85 90 95	
55	acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag gtg	336
	Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val	
	100 105 110	
55	aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc atc	384
	Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile	
	115 120 125	

	gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac	432
	Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn	
	130 135 140	
5	tac aac agc cac aac gtc tat atc atg gcc gac aag cag	471
	Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln	
	145 150 155	
10		
	YFP F1DX, Y66F mutation	
	SEQ ID NOS:490 & 491	
15	atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg	48
	Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu	
	1 5 10 15	
20	gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc	96
	Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly	
	20 25 30	
25	gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc	144
	Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile	
	35 40 45	
30	tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc	192
	Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr	
	50 55 60	
35	ttc ggc ttc ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag	240
	Phe Gly Phe Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys	
	65 70 75 80	
40	cgg cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag	288
	Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu	
	85 90 95	
45	cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag	336
	Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu	
	100 105 110	
50	gtg aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc	384
	Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly	
	115 120 125	
55	atc gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac	432
	Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr	
	130 135 140	
60	aac tac aac agc cac aac gtc tat atc atg gcc gac aag cag	474
	Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln	
	145 150 155	

YFP F1DX, Y66F mutation, pos. 1 Met removed  
SEQ ID NOS:492 & 493

5	gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val 1 5 10 15	48
10	gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu 20 25 30	96
15	ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc tgc Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys 35 40 45	144
20	acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ttc Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe 50 55 60	192
25	ggc ttc ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag cgg Gly Phe Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg 65 70 75 80	240
30	cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg 85 90 95	288
35	acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag gtg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val 100 105 110	336
40	aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc atc Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile 115 120 125	384
45	gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn 130 135 140	432
50	tac aac agc cac aac gtc tat atc atg gcc gac aag cag Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln 145 150 155	471

YFP F1DX, Q69K mutation  
SEQ ID NOS:494 & 495

50	atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu 1 5 10 15	48
55	gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly 20 25 30	96



	gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc	144
	Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile	
	35 40 45	
5	tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc	192
	Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr	
	50 55 60	
10	ttc ggc tac ggc ctg aag tgc ttc gcc cgc tac ccc gac cac atg aag	240
	Phe Gly Tyr Gly Leu Lys Cys Phe Ala Arg Tyr Pro Asp His Met Lys	
	65 70 75 80	
15	cgg cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag	288
	Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu	
	85 90 95	
20	cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag	336
	Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu	
	100 105 110	
25	gtg aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc	384
	Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly	
	115 120 125	
30	atc gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac	432
	Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr	
	130 135 140	
35	aac tac aac agc cac aac gtc tat atc atg gcc gac aag cag	474
	Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln	
	145 150 155	
40	YFP F1DX, Q69K mutation, pos. 1 Met removed	
	SEQ ID NOS:496 & 497	
45	gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc	48
	Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val	
	1 5 10 15	
50	gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag	96
	Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu	
	20 25 30	
55	ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc tgc	144
	Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys	
	35 40 45	
60	acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ttc	192
	Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe	
	50 55 60	
65	ggc tac ggc ctg aag tgc ttc gcc cgc tac ccc gac cac atg aag cgg	240
	Gly Tyr Gly Leu Lys Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg	
	65 70 75 80	

	cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc	288
	His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg	
	85 90 95	
5	acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag gtg	336
	Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val	
	100 105 110	
10	aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc atc	384
	Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile	
	115 120 125	
15	gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac	432
	Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn	
	130 135 140	
20	tac aac agc cac aac gtc tat atc atg gcc gac aag cag	471
	Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln	
	145 150 155	
citrine F1DX, V68L, Q69M mutations		
SEQ ID NOS:498 & 499		
25	atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg	48
	Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu	
	1 5 10 15	
30	gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc	96
	Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly	
	20 25 30	
35	gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc	144
	Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile	
	35 40 45	
40	tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc	192
	Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr	
	50 55 60	
45	ttc ggc tac ggc ctg atg tgc ttc gcc cgc tac ccc gac cac atg aag	240
	Phe Gly Tyr Gly Leu Met Cys Phe Ala Arg Tyr Pro Asp His Met Lys	
	65 70 75 80	
50	cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag	336
	Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu	
	100 105 110	
55	gtg aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc	384
	Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly	
	115 120 125	

	atc gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac	432
	Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr	
	130 135 140	
5	aac tac aac agc cac aac gtc tat atc atg gcc gac aag cag	474
	Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln	
	145 150 155	
10		
	citrine F1DX, V68L, Q69M mutations, and pos. 1 Met removed	
	SEQ ID NOS:500 & 501	
15	gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc	48
	Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val	
	1 5 10 15	
20	gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag	96
	Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu	
	20 25 30	
25	ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc tgc	144
	Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys	
	35 40 45	
30	acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ttc	192
	Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe	
	50 55 60	
35	ggc tac ggc ctg atg tgc ttc gcc cgc tac ccc gac cac atg aag cgg	240
	Gly Tyr Gly Leu Met Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg	
	65 70 75 80	
40	cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc	288
	His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg	
	85 90 95	
45	acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag gtg	336
	Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val	
	100 105 110	
50	aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc atc	384
	Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile	
	115 120 125	
55	gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac	432
	Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn	
	130 135 140	
60	tac aac agc cac aac gtc tat atc atg gcc gac aag cag	471
	Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln	
	145 150 155	

55

CFP F1DX, F64L mutation  
SEQ ID NOS:502 & 503

5	atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu 1 5 10 15	48
10	gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly 20 25 30	96
15	gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile 35 40 45	144
20	tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr 50 55 60	192
25	ctg ggc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag Leu Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys 65 70 75 80	240
30	cgg cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu 85 90 95	288
35	cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu 100 105 110	336
40	gtg aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly 115 120 125	384
45	atc gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr 130 135 140	432
50	aac tac aac agc cac aac gtc tat atc atg gcc gac aag cag Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln 145 150 155	474

CFP F1DX, F64L mutation, pos. 1 Met removed  
SEQ ID NOS:504 & 505

50	gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val 1 5 10 15	48
55	gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu 20 25 30	96

	ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc tgc	144
	Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys	
	35 40 45	
5	acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ctg	192
	Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Leu	
	50 55 60	
10	ggc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag cgg	240
	Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg	
	65 70 75 80	
15	cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc	288
	His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg	
	85 90 95	
20	acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag gtg	336
	Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val	
	100 105 110	
25	aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc atc	384
	Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile	
	115 120 125	
30	gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac	432
	Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn	
	130 135 140	
35	tac aac agc cac aac gtc tat atc atg gcc gac aag cag	471
	Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln	
	145 150 155	
40	CFP F1DX, F64L, S65T, Y66W mutations	
	SEQ ID NOS:506 & 507	
45	atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg	48
	Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu	
	1 5 10 15	
50	gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc	96
	Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly	
	20 25 30	
55	gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc	144
	Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile	
	35 40 45	
60	tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc	192
	Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr	
	50 55 60	
65	ctg acc tgg ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag	240
	Leu Thr Trp Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys	
	65 70 75 80	

	cgg cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag	288
	Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu	
	85 90 95	
5	cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag	336
	Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu	
	100 105 110	
10	gtg aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc	384
	Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly	
	115 120 125	
15	atc gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac	432
	Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr	
	130 135 140	
20	aac tac aac agc cac aac gtc tat atc atg gcc gac aag cag	474
	Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln	
	145 150 155	
	CFP F1DX, F64L,S65T,Y66W mutations, and pos. 1 Met removed	
25	SEQ ID NOS:508 & 509	
	gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc	48
	Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val	
	1 5 10 15	
30	gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag	96
	Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu	
	20 25 30	
35	ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc tgc	144
	Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys	
	35 40 45	
40	acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ctg	192
	Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Leu	
	50 55 60	
45	acc tgg ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag cgg	240
	Thr Trp Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg	
	65 70 75 80	
	cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc	288
	His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg	
	85 90 95	
50	acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag gtg	336
	Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val	
	100 105 110	
55	aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc atc	384
	Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile	
	115 120 125	

	gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac	432
	Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn	
	130 135 140	
5	tac aac agc cac aac gtc tat atc atg gcc gac aag cag	471
	Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln	
	145 150 155	
10		
	CFP F1DX, Y66W mutation	
	SEQ ID NOS:510 & 511	
15	atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg	48
	Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu	
	1 5 10 15	
20	gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc	96
	Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly	
	20 25 30	
25	gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc	144
	Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile	
	35 40 45	
30	tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc	192
	Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr	
	50 55 60	
35	ttc ggc tgg ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag	240
	Phe Gly Trp Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys	
	65 70 75 80	
40	cgg cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag	288
	Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu	
	85 90 95	
45	cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag	336
	Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu	
	100 105 110	
50	gtg aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc	384
	Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly	
	115 120 125	
55	atc gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac	432
	Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr	
	130 135 140	
60	aac tac aac agc cac aac gtc tat atc atg gcc gac aag cag	474
	Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln	
	145 150 155	

CFP F1DX,Y66W mutation, and pos. 1 Met removed  
SEQ ID NOS:512 & 513

5	gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val 1 5 10 15	48
10	gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu 20 25 30	96
15	ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc tgc Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys 35 40 45	144
20	acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ttc Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe 50 55 60	192
25	ggc tgg ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag cgg Gly Trp Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg 65 70 75 80	240
30	cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg 85 90 95	288
35	acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag gtg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val 100 105 110	336
40	aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc atc Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile 115 120 125	384
45	gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn 130 135 140	432
50	tac aac agc cac aac gtc tat atc atg gcc gac aag cag Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln 145 150 155	471

CFP F1DX, Y66W,N146I mutations  
SEQ ID NOS:514 & 515

50	atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu 1 5 10 15	48
55	gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly 20 25 30	96



	gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc	144
	Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile	
	35 40 45	
5	tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc	192
	Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr	
	50 55 60	
10	ttc ggc tgg ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag	240
	Phe Gly Trp Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys	
	65 70 75 80	
15	cgg cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag	288
	Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu	
	85 90 95	
20	cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag	336
	Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu	
	100 105 110	
25	gtg aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc	384
	Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly	
	115 120 125	
30	atc gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac	432
	Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr	
	130 135 140	
35	aac tac atc agc cac aac gtc tat atc atg gcc gac aag cag	474
	Asn Tyr Ile Ser His Asn Val Tyr Ile Met Ala Asp Lys	
	145 150 155	
40	CFP F1DX, Y66W,N146I mutations, pos. 1 Met removed	
	SEQ ID NOS:516 & 517	
45	gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc	48
	Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val	
	1 5 10 15	
50	gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag	96
	Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu	
	20 25 30	
55	ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc tgc	144
	Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys	
	35 40 45	
60	acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ttc	192
	Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe	
	50 55 60	
65	ggc tgg ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag cgg	240
	Gly Trp Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg	
	65 70 75 80	

	cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc	288
	His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg	
	85 90 95	
5	acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag gtg	336
	Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val	
	100 105 110	
10	aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc atc	384
	Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile	
	115 120 125	
15	gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac	432
	Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn	
	130 135 140	
20	tac atc agc cac aac gtc tat atc atg gcc gac aag cag	471
	Tyr Ile Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln	
	145 150 155	
CFP F1DX, Y66W, M153T mutations		
SEQ ID NOS:518 & 519		
25	atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg	48
	Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu	
	1 5 10 15	
30	gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc	96
	Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly	
	20 25 30	
35	gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc	144
	Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile	
	35 40 45	
40	tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc	192
	Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr	
	50 55 60	
45	ttc ggc tgg ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag	240
	Phe Gly Trp Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys	
	65 70 75 80	
50	cgg cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag	288
	Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu	
	85 90 95	
55	cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag	336
	Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu	
	100 105 110	
55	gtg aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc	384
	Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly	
	115 120 125	

	atc gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac	432
	Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr	
	130 135 140	
5	aac tac aac agc cac aac gtc tat atc acc gcc gac aag cag	474
	Asn Tyr Asn Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln	
	145 150 155	
10		
	CFP F1DX, Y66W, M153T mutations, pos. 1 Met removed	
	SEQ ID NOS:520 & 521	
15	gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc	48
	Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val	
	1 5 10 15	
20	gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag	96
	Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu	
	20 25 30	
25	ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc tgc	144
	Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys	
	35 40 45	
30	acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ttc	192
	Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe	
	50 55 60	
35	ggc tgg ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag cgg	240
	Gly Trp Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg	
	65 70 75 80	
40	cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc	288
	His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg	
	85 90 95	
45	acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag gtg	336
	Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val	
	100 105 110	
50	aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc atc	384
	Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile	
	115 120 125	
55	gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac	432
	Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn	
	130 135 140	
60	tac aac agc cac aac gtc tat atc acc gcc gac aag cag	471
	Tyr Asn Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln	
	145 150 155	

CFP F1DX, N146I mutation  
SEQ ID NOS:522 & 523

5	atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu	48
	1 5 10 15	
10	gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly	96
	20 25 30	
15	gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile	144
	35 40 45	
20	tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr	192
	50 55 60	
25	ttc ggc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag Phe Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys	240
	65 70 75 80	
30	cgg cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu	288
	85 90 95	
35	cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu	336
	100 105 110	
40	gtg aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly	384
	115 120 125	
45	atc gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr	432
	130 135 140	
50	aac tac atc agc cac aac gtc tat atc atg gcc gac aag cag Asn Tyr Ile Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln	474
	145 150 155	

CFP F1DX, N146I mutation, pos. 1 Met removed  
SEQ ID NOS:524 & 525

50	gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val	48
	1 5 10 15	
55	gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu	96
	20 25 30	

	ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc tgc	144
	Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys	
	35 40 45	
5	acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ttc	192
	Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe	
	50 55 60	
10	ggc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag cgg	240
	Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg	
	65 70 75 80	
15	cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc	288
	His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg	
	85 90 95	
20	acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag gtg	336
	Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val	
	100 105 110	
25	aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc atc	384
	Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile	
	115 120 125	
30	gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac	432
	Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn	
	130 135 140	
35	tac atc agc cac aac gtc tat atc atg gcc gac aag cag	471
	Tyr Ile Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln	
	145 150 155	
40	CFP F1DX, M153T mutation	
	SEQ ID NOS:526 & 527	
45	atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg	48
	Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu	
	1 5 10 15	
50	gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc	96
	Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly	
	20 25 30	
55	gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc	144
	Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile	
	35 40 45	
60	tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc	192
	Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr	
	50 55 60	
65	ttc ggc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag	240
	Phe Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys	
	65 70 75 80	

	cgg	cac	gac	ttc	ttc	aag	tcc	gcc	atg	ccc	gaa	ggc	tac	gtc	cag	gag	288
	Arg	His	Asp	Phe	Phe	Lys	Ser	Ala	Met	Pro	Glu	Gly	Tyr	Val	Gln	Glu	
				85						90					95		
5	cgc	acc	atc	ttc	ttc	aag	gac	gac	ggc	aac	tac	aag	acc	cgc	gcc	gag	336
	Arg	Thr	Ile	Phe	Phe	Lys	Asp	Asp	Gly	Asn	Tyr	Lys	Thr	Arg	Ala	Glu	
				100					105					110			
10	gtg	aag	ttc	gag	ggc	gac	acc	ctg	gtg	aac	cgc	atc	gag	ctg	aag	ggc	384
	Val	Lys	Phe	Glu	Gly	Asp	Thr	Leu	Val	Asn	Arg	Ile	Glu	Leu	Lys	Gly	
			115					120					125				
15	atc	gac	ttc	aag	gag	gac	ggc	aac	atc	ctg	ggg	cac	aag	ctg	gag	tac	432
	Ile	Asp	Phe	Lys	Glu	Asp	Gly	Asn	Ile	Leu	Gly	His	Lys	Leu	Glu	Tyr	
		130					135					140					
20	aac	tac	aac	agc	cac	aac	gtc	tat	atc	acc	gcc	gac	aag	cag			474
	Asn	Tyr	Asn	Ser	His	Asn	Val	Tyr	Ile	Thr	Ala	Asp	Lys	Gln			
		145				150					155						
CFP F1DX, M153T mutation, pos. 1 Met removed																	
SEQ ID NOS:528 & 529																	
25	gtg	agc	aag	ggc	gag	gag	ctg	ttc	acc	ggg	gtg	gtg	ccc	atc	ctg	gtc	48
	Val	Ser	Lys	Gly	Glu	Glu	Leu	Phe	Thr	Gly	Val	Val	Pro	Ile	Leu	Val	
	1				5					10					15		
30	gag	ctg	gac	ggc	gac	gta	aac	ggc	cac	aag	ttc	agc	gtg	tcc	ggc	gag	96
	Glu	Leu	Asp	Gly	Asp	Val	Asn	Gly	His	Lys	Phe	Ser	Val	Ser	Gly	Glu	
				20					25					30			
35	ggc	gag	ggc	gat	gcc	acc	tac	ggc	aag	ctg	acc	ctg	aag	ttc	atc	tgc	144
	Gly	Glu	Gly	Asp	Ala	Thr	Tyr	Gly	Lys	Leu	Thr	Leu	Lys	Phe	Ile	Cys	
			35					40					45				
40	acc	acc	ggc	aag	ctg	ccc	gtg	ccc	tgg	ccc	acc	ctc	gtg	acc	acc	ttc	192
	Thr	Thr	Gly	Lys	Leu	Pro	Val	Pro	Trp	Pro	Thr	Leu	Val	Thr	Thr	Phe	
		50					55					60					
45	ggc	tac	ggc	ctg	cag	tgc	ttc	gcc	cgc	tac	ccc	gac	cac	atg	aag	cgg	240
	Gly	Tyr	Gly	Leu	Gln	Cys	Phe	Ala	Arg	Tyr	Pro	Asp	His	Met	Lys	Arg	
		65			70					75					80		
50	cac	gac	ttc	ttc	aag	tcc	gcc	atg	ccc	gaa	ggc	tac	gtc	cag	gag	cgc	288
	His	Asp	Phe	Phe	Lys	Ser	Ala	Met	Pro	Glu	Gly	Tyr	Val	Gln	Glu	Arg	
				85					90					95			
55	acc	atc	ttc	ttc	aag	gac	gac	ggc	aac	tac	aag	acc	cgc	gcc	gag	gtg	336
	Thr	Ile	Phe	Phe													

	gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac	432
	Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn	
	130 135 140	
5	tac aac agc cac aac gtc tat atc acc gcc gac aag cag	471
	Tyr Asn Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln	
	145 150 155	
10		
	CFP F1DX, N146I, M153T mutations	
	SEQ ID NOS:530 & 531	
15	atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg	48
	Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu	
	1 5 10 15	
20	gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc	96
	Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly	
	20 25 30	
25	gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc	144
	Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile	
	35 40 45	
30	tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc	192
	Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr	
	50 55 60	
35	ttc ggc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag	240
	Phe Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys	
	65 70 75 80	
40	cgg cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag	288
	Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu	
	85 90 95	
45	cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag	336
	Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu	
	100 105 110	
50	gtg aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc	384
	Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly	
	115 120 125	
55	atc gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac	432
	Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr	
	130 135 140	
60	aac tac atc agc cac aac gtc tat atc acc gcc gac aag cag	474
	Asn Tyr Ile Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln	
	145 150 155	

CFP F1DX, N146I,M153T mutations, pos. 1 Met removed  
SEQ ID NOS:532 & 533

5	gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val 1 5 10 15	48
10	gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu 20 25 30	96
15	ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc tgc Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys 35 40 45	144
20	acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ttc Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe 50 55 60	192
25	ggc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag cgg Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg 65 70 75 80	240
30	cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg 85 90 95	288
35	acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag gtg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val 100 105 110	336
40	aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc atc Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile 115 120 125	384
45	gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn 130 135 140	432
50	tac atc agc cac aac gtc tat atc acc gcc gac aag cag Tyr Ile Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln 145 150 155	471

CFP F1DX, Y66W, N146I,M153T mutations  
SEQ ID NOS:534 & 535

50	atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu 1 5 10 15	48
55	gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly 20 25 30	96
60	gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile 35 40 45	144



	tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc	192
	Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr	
	50 55 60	
5	ttc ggc tgg ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag	240
	Phe Gly Trp Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys	
	65 70 75 80	
10	cgg cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag	288
	Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu	
	85 90 95	
15	cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag	336
	Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu	
	100 105 110	
20	gtg aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc	384
	Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly	
	115 120 125	
25	atc gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac	432
	Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr	
	130 135 140	
30	aac tac atc agc cac aac gtc tat atc acc gcc gac aag cag	474
	Asn Tyr Ile Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln	
	145 150 155	
30	CFP F1DX, Y66W, N146I, M153T mutations, and pos. 1 Met removed	
	SEQ ID NOS:536 & 537	
35	gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc	48
	Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val	
	1 5 10 15	
40	gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag	96
	Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu	
	20 25 30	
45	ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc tgc	144
	Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys	
	35 40 45	
50	acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ttc	192
	Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe	
	50 55 60	
50	ggc tgg ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag cgg	240
	Gly Trp Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg	
	65 70 75 80	
55	cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc	288
	His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg	
	85 90 95	

	acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag gtg	336
	Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val	
	100 105 110	
5	aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc atc	384
	Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile	
	115 120 125	
10	gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac	432
	Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn	
	130 135 140	
	tac atc agc cac aac gtc tat atc acc gcc gac aag cag	471
	Tyr Ile Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln	
15	145 150 155	
20	CFP F1DX, S65A mutation SEQ ID NOS:538 & 539	
	atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg	48
	Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu	
	1 5 10 15	
25	gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc	96
	Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly	
	20 25 30	
30	gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc	144
	Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile	
	35 40 45	
35	tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc	192
	Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr	
	50 55 60	
40	ttc gcc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag	240
	Phe Ala Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys	
	65 70 75 80	
	cgg cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag	288
	Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu	
	85 90 95	
45	cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag	336
	Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu	
	100 105 110	
50	gtg aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc	384
	Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly	
	115 120 125	
55	atc gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac	432
	Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr	
	130 135 140	



	gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc	96
	Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly	
	20 25 30	
5	gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc	144
	Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile	
	35 40 45	
10	tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc	192
	Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr	
	50 55 60	
15	ttc gcc tgg ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag	240
	Phe Ala Trp Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys	
	65 70 75 80	
20	cgg cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag	288
	Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu	
	85 90 95	
25	cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag	336
	Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu	
	100 105 110	
30	gtg aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc	384
	Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly	
	115 120 125	
35	atc gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac	432
	Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr	
	130 135 140	
40	aac tac aac agc cac aac gtc tat atc atg gcc gac aag cag	474
	Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln	
	145 150 155	
40	CFP F1DX, S65A,Y66W, S72A mutations, pos. 1 Met removed	
	SEQ ID NOS:544 & 545	
45	gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc	48
	Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val	
	1 5 10 15	
50	gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag	96
	Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu	
	20 25 30	
55	ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc tgc	144
	Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys	
	35 40 45	
60	acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ttc	192
	Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe	
	50 55 60	

	gcc tgg ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag cgg	240
	Ala Trp Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg	
	65 70 75 80	
5		
	cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc	288
	His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg	
	85 90 95	
10		
	acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag gtg	336
	Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val	
	100 105 110	
15		
	aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc atc	384
	Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile	
	115 120 125	
20		
	gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac	432
	Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn	
	130 135 140	
25		
	tac aac agc cac aac gtc tat atc atg gcc gac aag cag	471
	Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln	
	145 150 155	
	BFP F1DX, Y66H mutation	
	SEQ ID NOS:546 & 547	
30		
	atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg	48
	Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu	
	1 5 10 15	
35		
	gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc	96
	Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly	
	20 25 30	
40		
	gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc	144
	Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile	
	35 40 45	
45		
	tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc	192
	Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr	
	50 55 60	
50		
	ttc ggc cac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag	240
	Phe Gly His Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys	
	65 70 75 80	
55		
	cgg cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag	288
	Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu	
	85 90 95	
55		
	cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag	336
	Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu	
	100 105 110	

	gtg aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc	384
	Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly	
	115 120 125	
5	atc gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac	432
	Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr	
	130 135 140	
10	aac tac aac agc cac aac gtc tat atc atg gcc gac aag cag	474
	Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln	
	145 150 155	
15	BFP F1DX, Y66H mutation, pos. 1 Met removed	
	SEQ ID NOS:548 & 549	
	gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc	48
	Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val	
	1 5 10 15	
20	gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag	96
	Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu	
	20 25 30	
25	ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc tgc	144
	Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys	
	35 40 45	
30	acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ttc	192
	Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe	
	50 55 60	
35	ggc cac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag cgg	240
	Gly His Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg	
	65 70 75 80	
	cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc	288
	His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg	
	85 90 95	
40	acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag gtg	336
	Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val	
	100 105 110	
45	aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc atc	384
	Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile	
	115 120 125	
50	gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac	432
	Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn	
	130 135 140	
55	tac aac agc cac aac gtc tat atc atg gcc gac aag cag	471
	Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln	
	145 150 155	

BFP F1DX, F64L,Y66H mutations  
SEQ ID NOS:550 & 551

5	atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu	48
	1 5 10 15	
10	gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly	96
	20 25 30	
15	gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile	144
	35 40 45	
20	tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr	192
	50 55 60	
25	ctc ggc cac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag Leu Gly His Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys	240
	65 70 75 80	
30	cgg cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu	288
	85 90 95	
35	cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu	336
	100 105 110	
40	gtg aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly	384
	115 120 125	
45	atc gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr	432
	130 135 140	
50	aac tac aac agc cac aac gtc tat atc atg gcc gac aag cag Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln	474
	145 150 155	

BFP F1DX, F64L,Y66H mutations, pos. 1 Met removed  
SEQ ID NOS:552 & 553

50	gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val	48
	1 5 10 15	
55	gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu	96
	20 25 30	

	ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc tgc	144
	Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys	
	35 40 45	
5	acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ctc	192
	Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Leu	
	50 55 60	
10	ggc cac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag cgg	240
	Gly His Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg	
	65 70 75 80	
15	cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc	288
	His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg	
	85 90 95	
20	acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag gtg	336
	Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val	
	100 105 110	
25	aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc atc	384
	Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile	
	115 120 125	
30	gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac	432
	Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn	
	130 135 140	
35	tac aac agc cac aac gtc tat atc atg gcc gac aag cag	471
	Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln	
	145 150 155	
35	BFP F1DX, F64L, Y66H, Y145F mutations	
	SEQ ID NOS:554 & 555	
40	atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg	48
	Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu	
	1 5 10 15	
45	gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc	96
	Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly	
	20 25 30	
50	gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc	144
	Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile	
	35 40 45	
55	tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc	192
	Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr	
	50 55 60	
55	ctc ggc cac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag	240
	Leu Gly His Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys	
	65 70 75 80	



	cgg cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag	288
	Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu	
	85 90 95	
5	cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag	336
	Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu	
	100 105 110	
10	gtg aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc	384
	Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly	
	115 120 125	
15	atc gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac	432
	Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr	
	130 135 140	
20	aac ttc aac agc cac aac gtc tat atc atg gcc gac aag cag	474
	Asn Phe Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln	
	145 150 155	
BFP F1DX, F64L, Y66H, Y145F mutations and pos. 1 Met removed		
SEQ ID NOS:556 & 557		
25	gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc	48
	Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val	
	1 5 10 15	
30	gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag	96
	Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu	
	20 25 30	
35	ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc tgc	144
	Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys	
	35 40 45	
40	acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ctc	192
	Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Leu	
	50 55 60	
45	ggc cac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag cgg	240
	Gly His Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg	
	65 70 75 80	
50	cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc	288
	His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg	
	85 90 95	
55	acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag gtg	336
	Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val	
	100 105 110	
55	aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc atc	384
	Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile	
	115 120 125	

	gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac	432
	Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn	
	130 135 140	
5	ttc aac agc cac aac gtc tat atc atg gcc gac aag cag	471
	Phe Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln	
	145 150 155	
10		
	BFP F1DX, Y145F mutation	
	SEQ ID NOS:558 & 559	
15	atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg	48
	Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu	
	1 5 10 15	
20	gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc	96
	Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly	
	20 25 30	
25	gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc	144
	Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile	
	35 40 45	
30	tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc	192
	Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr	
	50 55 60	
35	ttc ggc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag	240
	Phe Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys	
	65 70 75 80	
40	cgg cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag	288
	Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu	
	85 90 95	
40	cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag	336
	Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu	
	100 105 110	
45	gtg aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc	384
	Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly	
	115 120 125	
50	atc gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac	432
	Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr	
	130 135 140	
55	aac ttc aac agc cac aac gtc tat atc atg gcc gac aag cag	474
	Asn Phe Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln	
	145 150 155	

BFP F1DX, Y145F mutation and pos. 1 Met removed  
SEQ ID NOS:560 & 561

5	gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val 1 5 10 15	48
10	gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu 20 25 30	96
15	ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc tgc Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys 35 40 45	144
20	acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ttc Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe 50 55 60	192
25	ggc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag cgg Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg 65 70 75 80	240
30	cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg 85 90 95	288
35	acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag gtg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val 100 105 110	336
40	aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc atc Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile 115 120 125	384
45	gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn 130 135 140	432
50	ttc aac agc cac aac gtc tat atc atg gcc gac aag cag Phe Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln 145 150 155	471

BFP F1DX, F46L,F64L,Y145F mutations  
SEQ ID NOS:562 & 563

50	atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu 1 5 10 15	48
55	gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly 20 25 30	96

	gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ctg atc	144
	Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Leu Ile	
	35 40 45	
5	tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc	192
	Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr	
	50 55 60	
10	ctg ggc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag	240
	Leu Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys	
	65 70 75 80	
15	cgg cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag	288
	Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu	
	85 90 95	
20	cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag	336
	Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu	
	100 105 110	
25	gtg aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc	384
	Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly	
	115 120 125	
30	atc gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac	432
	Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr	
	130 135 140	
35	aac ttc aac agc cac aac gtc tat atc atg gcc gac aag cag	474
	Asn Phe Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln	
	145 150 155	
40	BFP F1DX, F46L, F64L, Y145F mutations, and pos. 1 Met removed SEQ ID NOS:564 & 565	
40	gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc	48
	Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val	
	1 5 10 15	
45	gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag	96
	Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu	
	20 25 30	
50	ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ctg atc tgc	144
	Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Leu Ile Cys	
	35 40 45	
55	acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ctg	192
	Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Leu	
	50 55 60	
55	ggc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag cgg	240
	Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg	
	65 70 75 80	

	cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc	288
	His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg	
	85 90 95	
5	acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag gtg	336
	Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val	
	100 105 110	
10	aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc atc	384
	Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile	
	115 120 125	
15	gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac	432
	Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn	
	130 135 140	
20	ttc aac agc cac aac gtc tat atc atg gcc gac aag cag	471
	Phe Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln	
	145 150 155	
25	Venus F1DX, F46L mutation	
	SEQ ID NOS:566 & 567	
30	atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg	48
	Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu	
	1 5 10 15	
35	gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc	96
	Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly	
	20 25 30	
40	gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ctg atc	144
	Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Leu Ile	
	35 40 45	
45	tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc	192
	Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr	
	50 55 60	
50	ttc ggc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag	240
	Phe Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys	
	65 70 75 80	
55	cgg cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag	288
	Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu	
	85 90 95	
60	cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag	336
	Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu	
	100 105 110	
65	gtg aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc	384
	Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly	
	115 120 125	

atc gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac 432  
 Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr  
 130 135 140

5

aac tac aac agc cac aac gtc tat atc atg gcc gac aag cag 474  
 Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln  
 145 150 155

10

Venus F1DX, F46L mutation, pos. 1 Met removed  
 SEQ ID NOS:568 & 569

15

gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc 48  
 Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val  
 1 5 10 15

20

gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag 96  
 Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu  
 20 25 30

25

ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ctg atc tgc 144  
 Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Leu Ile Cys  
 35 40 45

30

acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ttc 192  
 Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe  
 50 55 60

35

ggc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag cgg 240  
 Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg  
 65 70 75 80

40

cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc 288  
 His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg  
 85 90 95

45

acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag gtg 336  
 Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val  
 100 105 110

50

aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc atc 384  
 Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile  
 115 120 125

55

gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac 432  
 Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn  
 130 135 140

tac aac agc cac aac gtc tat atc atg gcc gac aag cag 471  
 Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln  
 145 150 155

Venus F1DX, F46L,F64L mutations  
SEQ ID NOS:570 & 571

5	atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu 1 5 10 15	48
10	gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly 20 25 30	96
15	gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ctg atc Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Leu Ile 35 40 45	144
20	tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr 50 55 60	192
25	ctg ggc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag Leu Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys 65 70 75 80	240
30	cgg cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu 85 90 95	288
35	cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu 100 105 110	336
40	gtg aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly 115 120 125	384
45	atc gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr 130 135 140	432
50	aac tac aac agc cac aac gtc tat atc atg gcc gac aag cag Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln 145 150 155	474

Venus F1DX, F46L,F64L mutations, pos. 1 Met removed  
SEQ ID NOS:572 & 573

50	gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val 1 5 10 15	48
55	gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu 20 25 30	96

	ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ctg atc tgc	144
	Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Leu Ile Cys	
	35 40 45	
5	acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ctg	192
	Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Leu	
	50 55 60	
10	ggc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag cgg	240
	Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg	
	65 70 75 80	
15	cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc	288
	His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg	
	85 90 95	
20	acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag gtg	336
	Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val	
	100 105 110	
	aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc atc	384
	Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile	
	115 120 125	
25	gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac	432
	Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn	
	130 135 140	
30	tac aac agc cac aac gtc tat atc atg gcc gac aag cag	471
	Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln	
	145 150 155	
35	SEYFP F1DX, F64L,M153T mutations	
	SEQ ID NOS:574 & 575	
40	atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg	48
	Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu	
	1 5 10 15	
45	gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc	96
	Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly	
	20 25 30	
	gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc	144
	Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile	
	35 40 45	
50	tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc	192
	Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr	
	50 55 60	
55	ctg ggc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag	240
	Leu Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys	
	65 70 75 80	



	cgg cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag	288
	Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu	
	85 90 95	
5	cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag	336
	Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu	
	100 105 110	
10	gtg aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc	384
	Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly	
	115 120 125	
15	atc gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac	432
	Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr	
	130 135 140	
20	aac tac aac agc cac aac gtc tat atc acc gcc gac aag cag	474
	Asn Tyr Asn Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln	
	145 150 155	
25	SEYFP F1DX, F64L,M153T mutations, and pos. 1 Met removed	
	SEQ ID NOS:576 & 577	
30	gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc	48
	Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val	
	1 5 10 15	
35	gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag	96
	Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu	
	20 25 30	
40	ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc tgc	144
	Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys	
	35 40 45	
45	acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ctg	192
	Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Leu	
	50 55 60	
50	ggc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag cgg	240
	Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg	
	65 70 75 80	
55	cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc	288
	His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg	
	85 90 95	
60	acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag gtg	336
	Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val	
	100 105 110	
65	aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc atc	384
	Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile	
	115 120 125	

	gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac	432
	Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn	
	130 135 140	
5	tac aac agc cac aac gtc tat atc acc gcc gac aag cag	471
	Tyr Asn Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln	
	145 150 155	
10	Venus F1DX,F64L,M153T mutations	
	SEQ ID NOS:578 & 579	
15	atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg	48
	Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu	
	1 5 10 15	
20	gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc	96
	Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly	
	20 25 30	
25	gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc	144
	Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile	
	35 40 45	
30	tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc	192
	Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr	
	50 55 60	
35	ctg ggc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag	240
	Leu Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys	
	65 70 75 80	
40	cgg cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag	288
	Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu	
	85 90 95	
45	cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag	336
	Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu	
	100 105 110	
50	gtg aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc	384
	Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly	
	115 120 125	
55	atc gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac	432
	Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr	
	130 135 140	
60	aac tac aac agc cac aac gtc tat atc acc gcc gac aag cag	474
	Asn Tyr Asn Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln	
	145 150 155	

Venus F1DX, F64L, M153T mutations, pos. 1 Met removed  
SEQ ID NOS:580 & 581

5	gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val 1 5 10 15	48
10	gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu 20 25 30	96
15	ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc tgc Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys 35 40 45	144
20	acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctg gtg acc acc ctg Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Leu 50 55 60	192
25	ggc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag cgg Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg 65 70 75 80	240
30	cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg 85 90 95	288
35	acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag gtg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val 100 105 110	336
40	aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc atc Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile 115 120 125	384
45	gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn 130 135 140	432
50	tac aac agc cac aac gtc tat atc acc gcc gac aag cag Tyr Asn Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln 145 150 155	471

Venus F1DX, F46L, F64L, M153T mutations  
SEQ ID NOS:582 & 583

50	atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu 1 5 10 15	48
55	gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly 20 25 30	96

	gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ctg atc	144
	Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Leu Ile	
	35 40 45	
5	tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc	192
	Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr	
	50 55 60	
10	ctg ggc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag	240
	Leu Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys	
	65 70 75 80	
15	cgg cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag	288
	Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu	
	85 90 95	
20	cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag	336
	Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu	
	100 105 110	
25	gtg aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc	384
	Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly	
	115 120 125	
30	atc gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac	432
	Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr	
	130 135 140	
35	aac tac aac agc cac aac gtc tat atc acc gcc gac aag cag	474
	Asn Tyr Asn Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln	
	145 150 155	
40	Venus F1DX, F46L, F64L, M153T mutations, and pos. 1 Met removed SEQ ID NOS:584 & 585	
45	gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc	48
	Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val	
	1 5 10 15	
50	gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag	96
	Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu	
	20 25 30	
55	ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ctg atc tgc	144
	Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Leu Ile Cys	
	35 40 45	
60	acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ctg	192
	Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Leu	
	50 55 60	
65	ggc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag cgg	240
	Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg	
	65 70 75 80	

	cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc	288
	His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg	
	85 90 95	
5	acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag gtg	336
	Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val	
	100 105 110	
10	aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc atc	384
	Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile	
	115 120 125	
15	gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac	432
	Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn	
	130 135 140	
20	tac aac agc cac aac gtc tat atc acc gcc gac aag cag	471
	Tyr Asn Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln	
	145 150 155	
YFPF2DX, Met added @ posit. 1		
(YFP F2DX corresponds to aa residues 159-239 of YFP)		
25	SEQ ID NOS:586 & 587	
30	atg aag aac ggc atc aag gtg aac ttc aag atc cgc cac aac atc gag	48
	Met Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu	
	1 5 10 15	
35	gac ggc agc gtg cag ctc gcc gac cac tac cag cag aac acc ccc atc	96
	Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile	
	20 25 30	
40	ggc gac ggc ccc gtg ctg ctg ccc gac aac cac tac ctg agc tac cag	144
	Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Tyr Gln	
	35 40 45	
45	tcc gcc ctg agc aaa gac ccc aac gag aag cgc gat cac atg gtc ctg	192
	Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu	
	50 55 60	
50	ctg gag ttc gtg acc gcc gcc ggg atc act ctc ggc atg gac gag ctg	240
	Leu Glu Phe Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu	
	65 70 75 80	
55	tac aag	246
	Tyr Lys	
YFP F2DX, Y203F mutation		
SEQ ID NOS:588 & 589		
55	aag aac ggc atc aag gtg aac ttc aag atc cgc cac aac atc gag gac	48
	Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp	
	1 5 10 15	

	ggc agc gtg cag ctc gcc gac cac tac cag cag aac acc ccc atc ggc	96
	Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly	
	20 25 30	
5		
	gac ggc ccc gtg ctg ctg ccc gac aac cac tac ctg agc ttc cag tcc	144
	Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Phe Gln Ser	
	35 40 45	
10		
	gcc ctg agc aaa gac ccc aac gag aag cgc gat cac atg gtc ctg ctg	192
	Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu	
	50 55 60	
15		
	gag ttc gtg acc gcc gcc ggg atc act ctc ggc atg gac gag ctg tac	240
	Glu Phe Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr	
	65 70 75 80	
20		
	aag	243
	Lys	
25		
	YFP F2DX, Y203F mutation, and Met added @ pos. 1	
	SEQ ID NOS:590 & 591	
	atg aag aac ggc atc aag gtg aac ttc aag atc cgc cac aac atc gag	48
	Met Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu	
	1 5 10 15	
30		
	gac ggc agc gtg cag ctc gcc gac cac tac cag cag aac acc ccc atc	96
	Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile	
	20 25 30	
35		
	ggc gac ggc ccc gtg ctg ctg ccc gac aac cac tac ctg agc ttc cag	144
	Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Phe Gln	
	35 40 45	
40		
	tcc gcc ctg agc aaa gac ccc aac gag aag cgc gat cac atg gtc ctg	192
	Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu	
	50 55 60	
45		
	ctg gag ttc gtg acc gcc gcc ggg atc act ctc ggc atg gac gag ctg	240
	Leu Glu Phe Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu	
	65 70 75 80	
	tac aag	246
	Tyr Lys	
50		
	YFP F2DX, Y203H mutation	
	SEQ ID NOS:592 & 593	
	aag aac ggc atc aag gtg aac ttc aag atc cgc cac aac atc gag gac	48
55	Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp	
	1 5 10 15	

	ggc agc gtg cag ctc gcc gac cac tac cag cag aac acc ccc atc ggc	96
	Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly	
	20 25 30	
5	gac ggc ccc gtg ctg ctg ccc gac aac cac tac ctg agc cac cag tcc	144
	Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser His Gln Ser	
	35 40 45	
10	gcc ctg agc aaa gac ccc aac gag aag cgc gat cac atg gtc ctg ctg	192
	Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu	
	50 55 60	
15	gag ttc gtg acc gcc gcc ggg atc act ctc ggc atg gac gag ctg tac	240
	Glu Phe Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr	
	65 70 75 80	
	aag	243
	Lys	
20	YFP F2DX, Y203H mutation, and Met added @ pos. 1	
	SEQ ID NOS:594 & 595	
25	atg aag aac ggc atc aag gtg aac ttc aag atc cgc cac aac atc gag	48
	Met Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu	
	1 5 10 15	
30	gac ggc agc gtg cag ctc gcc gac cac tac cag cag aac acc ccc atc	96
	Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile	
	20 25 30	
35	ggc gac ggc ccc gtg ctg ctg ccc gac aac cac tac ctg agc cac cag	144
	Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser His Gln	
	35 40 45	
40	tcc gcc ctg agc aaa gac ccc aac gag aag cgc gat cac atg gtc ctg	192
	Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu	
	50 55 60	
45	ctg gag ttc gtg acc gcc gcc ggg atc act ctc ggc atg gac gag ctg	240
	Leu Glu Phe Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu	
	65 70 75 80	
50	tac aag	246
	Tyr Lys	
	CFP F2DX, Y203T mutation	
	SEQ ID NOS:596 & 597	
55	aag aac ggc atc aag gtg aac ttc aag atc cgc cac aac atc gag gac	48
	Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp	
	1 5 10 15	
60	ggc agc gtg cag ctc gcc gac cac tac cag cag aac acc ccc atc ggc	96
	Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly	
	20 25 30	

	gac ggc ccc gtg ctg ctg ccc gac aac cac tac ctg agc act cag tcc	144
	Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser	
	35 40 45	
5		
	gcc ctg agc aaa gac ccc aac gag aag cgc gat cac atg gtc ctg ctg	192
	Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu	
	50 55 60	
10		
	gag ttc gtg acc gcc gcc ggg atc act ctc ggc atg gac gag ctg tac	240
	Glu Phe Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr	
	65 70 75 80	
	aag	243
15	Lys	
20	CFP F2DX, Y203T mutation, and Met added @ pos. 1	
	SEQ ID NOS:598 & 599	
	atg aag aac ggc atc aag gtg aac ttc aag atc cgc cac aac atc gag	48
	Met Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu	
	1 5 10 15	
25		
	gac ggc agc gtg cag ctc gcc gac cac tac cag cag aac acc ccc atc	96
	Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile	
	20 25 30	
30		
	ggc gac ggc ccc gtg ctg ctg ccc gac aac cac tac ctg agc act cag	144
	Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln	
	35 40 45	
	tcc gcc ctg agc aaa gac ccc aac gag aag cgc gat cac atg gtc ctg	192
35	Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu	
	50 55 60	
	ctg gag ttc gtg acc gcc gcc ggg atc act ctc ggc atg gac gag ctg	240
	Leu Glu Phe Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu	
40	65 70 75 80	
	tac aag	246
	Tyr Lys	
45		
	CFP F2DX, V163A, Y203T mutations	
	SEQ ID NOS:600 & 601	
50		
	aag aac ggc atc aag gcc aac ttc aag atc cgc cac aac atc gag gac	48
	Lys Asn Gly Ile Lys Ala Asn Phe Lys Ile Arg His Asn Ile Glu Asp	
	1 5 10 15	
	ggc agc gtg cag ctc gcc gac cac tac cag cag aac acc ccc atc ggc	96
55	Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly	
	20 25 30	



	gac ggc ccc gtg ctg ctg ccc gac aac cac tac ctg agc acc cag tcc	144
	Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser	
	35 40 45	
5	gcc ctg agc aaa gac ccc aac gag aag cgc gat cac atg gtc ctg ctg	192
	Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu	
	50 55 60	
10	gag ttc gtg acc gcc gcc ggg atc act ctc ggc atg gac gag ctg tac	240
	Glu Phe Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr	
	65 70 75 80	
	aag	243
	Lys	
15		
	CFP F2DX, V163A,Y203T mutations, and Met added @ pos. 1	
	SEQ ID NOS:602 & 603	
20	atg aag aac ggc atc aag gcc aac ttc aag atc cgc cac aac atc gag	48
	Met Lys Asn Gly Ile Lys Ala Asn Phe Lys Ile Arg His Asn Ile Glu	
	1 5 10 15	
25	gac ggc agc gtg cag ctc gcc gac cac tac cag cag aac acc ccc atc	96
	Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile	
	20 25 30	
30	ggc gac ggc ccc gtg ctg ctg ccc gac aac cac tac ctg agc acc cag	144
	Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln	
	35 40 45	
	tcc gcc ctg agc aaa gac ccc aac gag aag cgc gat cac atg gtc ctg	192
	Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu	
35	50 55 60	
	ctg gag ttc gtg acc gcc gcc ggg atc act ctc ggc atg gac gag ctg	240
	Leu Glu Phe Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu	
	65 70 75 80	
40	tac aag	246
	Tyr Lys	
45		
	Venus F2DX, S175G mutation	
	SEQ ID NOS:604 & 605	
50	atg aag aac ggc atc aag gtg aac ttc aag atc cgc cac aac atc gag	48
	Met Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu	
	1 5 10 15	
55	gac ggc ggc gtg cag ctc gcc gac cac tac cag cag aac acc ccc atc	96
	Asp Gly Gly Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile	
	20 25 30	

	ggc gac ggc ccc gtg ctg ctg ccc gac aac cac tac ctg agc tac cag	144
	Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Tyr Gln	
	35 40 45	
5	tcc gcc ctg agc aaa gac ccc aac gag aag cgc gat cac atg gtc ctg	192
	Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu	
	50 55 60	
10	ctg gag ttc gtg acc gcc gcc ggg atc act ctc ggc atg gac gag ctg	240
	Leu Glu Phe Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu	
	65 70 75 80	
	tac aag	246
15	Tyr Lys	
Venus F2DX, S175G mutation, and Met added @ pos. 1		
SEQ ID NOS:606 & 607		
20	atg aag aac ggc atc aag gtg aac ttc aag atc cgc cac aac atc gag	48
	Met Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu	
	1 5 10 15	
25	gac ggc ggc gtg cag ctc gcc gac cac tac cag cag aac acc ccc atc	96
	Asp Gly Gly Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile	
	20 25 30	
30	ggc gac ggc ccc gtg ctg ctg ccc gac aac cac tac ctg agc tac cag	144
	Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Tyr Gln	
	35 40 45	
35	tcc gcc ctg agc aaa gac ccc aac gag aag cgc gat cac atg gtc ctg	192
	Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu	
	50 55 60	
40	ctg gag ttc gtg acc gcc gcc ggg atc act ctc ggc atg gac gag ctg	240
	Leu Glu Phe Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu	
	65 70 75 80	
	tac aag	246
	Tyr Lys	
45		
Venus F2DX, V163A,S175G mutations		
SEQ ID NOS:608 & 609		
50	aag aac ggc atc aag gcc aac ttc aag atc cgc cac aac atc gag gac	48
	Lys Asn Gly Ile Lys Ala Asn Phe Lys Ile Arg His Asn Ile Glu Asp	
	1 5 10 15	
55	ggc ggc gtg cag ctc gcc gac cac tac cag cag aac acc ccc atc ggc	96
	Gly Gly Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly	
	20 25 30	

	gac ggc ccc gtg ctg ctg ccc gac aac cac tac ctg agc tac cag tcc	144
	Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Tyr Gln Ser	
	35 40 45	
5	gcc ctg agc aaa gac ccc aac gag aag cgc gat cac atg gtc ctg ctg	192
	Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu	
	50 55 60	
10	gag ttc gtg acc gcc gcc ggg atc act ctc ggc atg gac gag ctg tac	240
	Glu Phe Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr	
	65 70 75 80	
	aag	243
15	Lys	
Venus F2DX, V163A, S175G mutations, and Met added @ pos. 1		
20	SEQ ID NOS:610 & 611	
	atg aag aac ggc atc aag gcc aac ttc aag atc cgc cac aac atc gag	48
	Met Lys Asn Gly Ile Lys Ala Asn Phe Lys Ile Arg His Asn Ile Glu	
	1 5 10 15	
25	gac ggc ggc gtg cag ctc gcc gac cac tac cag cag aac acc ccc atc	96
	Asp Gly Gly Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile	
	20 25 30	
30	ggc gac ggc ccc gtg ctg ctg ccc gac aac cac tac ctg agc tac cag	144
	Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Tyr Gln	
	35 40 45	
35	tcc gcc ctg agc aaa gac ccc aac gag aag cgc gat cac atg gtc ctg	192
	Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu	
	50 55 60	
40	ctg gag ttc gtg acc gcc gcc ggg atc act ctc ggc atg gac gag ctg	240
	Leu Glu Phe Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu	
	65 70 75 80	
	tac aag	246
	Tyr Lys	
45	YFP F1D, position 1 Met removed	
	(YFP F1D corresponds to aa residues 1-159 of YFP)	
	SEQ ID NOS:612 & 613	
50	gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc	48
	Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val	
	1 5 10 15	
55	gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag	96
	Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu	
	20 25 30	

	ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc tgc	144
	Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys	
	35 40 45	
5	acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ttc	192
	Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe	
	50 55 60	
10	ggc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag cgg	240
	Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg	
	65 70 75 80	
15	cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc	288
	His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg	
	85 90 95	
20	acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag gtg	336
	Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val	
	100 105 110	
	aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc atc	384
	Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile	
	115 120 125	
25	gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac	432
	Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn	
	130 135 140	
30	tac aac agc cac aac gtc tat atc atg gcc gac aag cag aag	474
	Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys	
	145 150 155	
35	YFP F1D, K79R mutation	
	SEQ ID NOS:614 & 615	
40	atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg	48
	Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu	
	1 5 10 15	
	gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc	96
	Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly	
	20 25 30	
45	gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc	144
	Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile	
	35 40 45	
50	tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc	192
	Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr	
	50 55 60	
55	ttc ggc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag	240
	Phe Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys	
	65 70 75 80	

	cgg cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag	288
	Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu	
	85 90 95	
5	cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag	336
	Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu	
	100 105 110	
10	gtg aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc	384
	Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly	
	115 120 125	
15	atc gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac	432
	Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr	
	130 135 140	
20	aac tac aac agc cac aac gtc tat atc atg gcc gac aag cag aag	477
	Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys	
	145 150 155	
YFP F1D, K79R mutation, Met @ pos. 1 removed		
SEQ ID NOS:616 & 617		
25	gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc	48
	Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val	
	1 5 10 15	
30	gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag	96
	Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu	
	20 25 30	
35	ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc tgc	144
	Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys	
	35 40 45	
40	acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ttc	192
	Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe	
	50 55 60	
45	ggc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag cgg	240
	Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg	
	65 70 75 80	
50	cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc	288
	His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg	
	85 90 95	
55	acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag gtg	336
	Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val	
	100 105 110	
55	aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc atc	384
	Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile	
	115 120 125	

	gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac	432
	Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn	
	130 135 140	
5	tac aac agc cac aac gtc tat atc atg gcc gac aag cag aag	474
	Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys	
	145 150 155	
10		
	YFP F1D, Y66F mutation	
	SEQ ID NOS:618 & 619	
15	atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg	48
	Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu	
	1 5 10 15	
20	gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc	96
	Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly	
	20 25 30	
25	gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc	144
	Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile	
	35 40 45	
30	tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc	192
	Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr	
	50 55 60	
35	ttc ggc ttc ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag	240
	Phe Gly Phe Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys	
	65 70 75 80	
40	cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag	336
	Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu	
	100 105 110	
45	gtg aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc	384
	Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly	
	115 120 125	
50	atc gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac	432
	Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr	
	130 135 140	
55	aac tac aac agc cac aac gtc tat atc atg gcc gac aag cag aag	477
	Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys	
	145 150 155	

YFP F1D, Y66F mutation, Met @ pos. 1 removed  
SEQ ID NOS:620 & 621

5	gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val 1 5 10 15	48
10	gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu 20 25 30	96
15	ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc tgc Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys 35 40 45	144
	acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ttc Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe 50 55 60	192
20	ggc ttc ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag cgg Gly Phe Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg 65 70 75 80	240
25	cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg 85 90 95	288
30	acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag gtg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val 100 105 110	336
35	aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc atc Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile 115 120 125	384
	gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn 130 135 140	432
40	tac aac agc cac aac gtc tat atc atg gcc gac aag cag aag Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys 145 150 155	474

45

YFP F1D, Q69K mutation  
SEQ ID NOS:622 & 623

50	atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu 1 5 10 15	48
55	gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly 20 25 30	96

	gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc	144
	Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile	
	35 40 45	
5	tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc	192
	Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr	
	50 55 60	
10	ttc ggc tac ggc ctg aag tgc ttc gcc cgc tac ccc gac cac atg aag	240
	Phe Gly Tyr Gly Leu Lys Cys Phe Ala Arg Tyr Pro Asp His Met Lys	
	65 70 75 80	
15	cgg cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag	288
	Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu	
	85 90 95	
20	cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag	336
	Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu	
	100 105 110	
25	gtg aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc	384
	Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly	
	115 120 125	
30	atc gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac	432
	Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr	
	130 135 140	
35	aac tac aac agc cac aac gtc tat atc atg gcc gac aag cag aag	477
	Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys	
	145 150 155	
40	gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc	48
	Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val	
	1 5 10 15	
45	gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag	96
	Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu	
	20 25 30	
50	ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc tgc	144
	Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys	
	35 40 45	
55	acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ttc	192
	Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe	
	50 55 60	
60	ggc tac ggc ctg aag tgc ttc gcc cgc tac ccc gac cac atg aag cgg	240
	Gly Tyr Gly Leu Lys Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg	
	65 70 75 80	

YFP F1D, Q69K mutation, Met @ pos. 1 removed  
SEQ ID NOS:624 & 625



	cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc	288														
	His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg															
	85 90 95															
5	acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag gtg	336														
	Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val															
	100 105 110															
10	aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc atc	384														
	Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile															
	115 120 125															
15	gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac	432														
	Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn															
	130 135 140															
20	tac aac agc cac aac gtc tat atc atg gcc gac aag cag aag	474														
	Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys															
	145 150 155															
	citrine F1D, V68L, Q69M mutations															
25	SEQ ID NOS:626 & 627															
	atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg	48														
	Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu															
	1 5 10 15															
30	gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc	96														
	Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly															
	20 25 30															
35	gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc	144														
	Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile															
	35 40 45															
40	tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc	192														
	Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr															
	50 55 60															
45	ttc ggc tac ggc ctg atg tgc ttc gcc cgc tac ccc gac cac atg aag	240														
	Phe Gly Tyr Gly Leu Met Cys Phe Ala Arg Tyr Pro Asp His Met Lys															
	65 70 75 80															
	cgg cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag	288														
	Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu															
	85 90 95															
50	cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag	336														
	Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu															
	100 105 110															
55	gtg aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc	384														
	Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly															
	115 120 125															

	atc gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac	432
	Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr	
	130 135 140	
5	aac tac aac agc cac aac gtc tat atc atg gcc gac aag cag aag	477
	Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys	
	145 150 155	
10		
	citrine F1D, V68L,Q69M mutations, Met @ pos.1 removed	
	SEQ ID NOS:628 & 629	
15	gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc	48
	Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val	
	1 5 10 15	
20	gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag	96
	Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu	
	20 25 30	
25	ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc tgc	144
	Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys	
	35 40 45	
30	acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ttc	192
	Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe	
	50 55 60	
35	ggc tac ggc ctg atg tgc ttc gcc cgc tac ccc gac cac atg aag cgg	240
	Gly Tyr Gly Leu Met Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg	
	65 70 75 80	
40	cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc	288
	His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg	
	85 90 95	
45	acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag gtg	336
	Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val	
	100 105 110	
50	aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc atc	384
	Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile	
	115 120 125	
55	gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac	432
	Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn	
	130 135 140	
60	tac aac agc cac aac gtc tat atc atg gcc gac aag cag aag	474
	Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys	
	145 150 155	

CFP F1D, F64L mutation  
SEQ ID NOS:630 & 631

5	atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu	48
	1 5 10 15	
10	gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly	96
	20 25 30	
15	gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile	144
	35 40 45	
	tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr	192
	50 55 60	
20	ctg ggc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag Leu Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys	240
	65 70 75 80	
25	cgg cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu	288
	85 90 95	
30	cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu	336
	100 105 110	
35	gtg aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly	384
	115 120 125	
	atc gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr	432
	130 135 140	
40	aac tac aac agc cac aac gtc tat atc atg gcc gac aag cag aag Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys	477
	145 150 155	

45

CFP F1D, F64L mutation, Met @ pos. 1 removed  
SEQ ID NOS:632 & 633

50	gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val	48
	1 5 10 15	
55	gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu	96
	20 25 30	

	ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc tgc	144
	Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys	
	35 40 45	
5	acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ctg	192
	Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Leu	
	50 55 60	
10	ggc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag cgg	240
	Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg	
	65 70 75 80	
15	cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc	288
	His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg	
	85 90 95	
20	acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag gtg	336
	Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val	
	100 105 110	
25	aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc atc	384
	Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile	
	115 120 125	
30	gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac	432
	Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn	
	130 135 140	
35	tac aac agc cac aac gtc tat atc atg gcc gac aag cag aag	474
	Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys	
	145 150 155	
35	YFP F1D, F46L mutation	
	SEQ ID NOS:634 & 635	
40	atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg	48
	Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu	
	1 5 10 15	
45	gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc	96
	Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly	
	20 25 30	
50	gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ctg atc	144
	Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Leu Ile	
	35 40 45	
55	tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc	192
	Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr	
	50 55 60	
55	ttc ggc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag	240
	Phe Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys	
	65 70 75 80	

	cgc cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag	288
	Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu	
	85 90 95	
5	cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag	336
	Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu	
	100 105 110	
10	gtg aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc	384
	Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly	
	115 120 125	
15	atc gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac	432
	Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr	
	130 135 140	
20	aac tac aac agc cac aac gtc tat atc atg gcc gac aag cag aag	477
	Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys	
	145 150 155	
25	YFP F1D, F46L mutation, Met @ pos. 1 removed	
	SEQ ID NOS:636 & 637	
30	gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc	48
	Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val	
	1 5 10 15	
35	gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag	96
	Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu	
	20 25 30	
40	ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ctg atc tgc	144
	Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Leu Ile Cys	
	35 40 45	
45	acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ttc	192
	Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe	
	50 55 60	
50	ggc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag cgg	240
	Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg	
	65 70 75 80	
55	cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc	288
	His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg	
	85 90 95	
60	acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag gtg	336
	Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val	
	100 105 110	
65	aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc atc	384
	Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile	
	115 120 125	

5      gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac      432  
       Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn  
           130                               135                               140

10      tac aac agc cac aac gtc tat atc atg gcc gac aag cag aag      474  
       Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys  
           145                               150                               155

15      atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg      48  
       Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu  
           1                               5                               10                               15

20      gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc      96  
       Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly  
                               20                               25                               30

25      gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ctg atc      144  
       Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Leu Ile  
                               35                               40                               45

30      tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc      192  
       Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr  
           50                               55                               60

35      ctg ggc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag      240  
       Leu Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys  
           65                               70                               75                               80

40      cgg cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag      288  
       Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu  
                               85                               90                               95

45      cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag      336  
       Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu  
                               100                               105                               110

50      gtg aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc      384  
       Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly  
                               115                               120                               125

55      atc gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac      432  
       Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr  
           130                               135                               140

60      aac tac aac agc cac aac gtc tat atc atg gcc gac aag cag aag      477  
       Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys  
           145                               150                               155

YFP F1D, F46L, F64L mutations, Met @ pos. 1 removed  
 SEQ ID NOS:640 & 641

5	gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val 1 5 10 15	48
10	gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu 20 25 30	96
15	ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ctg atc tgc Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Leu Ile Cys 35 40 45	144
20	acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ctg Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Leu 50 55 60	192
25	ggc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag cgg Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg 65 70 75 80	240
30	cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg 85 90 95	288
35	acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag gtg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val 100 105 110	336
40	aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc atc Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile 115 120 125	384
45	gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn 130 135 140	432
50	tac aac agc cac aac gtc tat atc atg gcc gac aag cag aag Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys 145 150 155	474

Venus F1D, F64L,M153T mutations  
 SEQ ID NOS:642 & 643

50	atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu 1 5 10 15	48
55	gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly 20 25 30	96
60	gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile 35 40 45	144

	tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc	192
	Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr	
	50 55 60	
5	ctg ggc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag	240
	Leu Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys	
	65 70 75 80	
10	cgg cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag	288
	Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu	
	85 90 95	
15	cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag	336
	Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu	
	100 105 110	
20	gtg aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc	384
	Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly	
	115 120 125	
25	atc gac ttc aag gag gac ggc aac atc ctg ggc cac aag ctg gag tac	432
	Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr	
	130 135 140	
	aac tac aac agc cac aac gtc tat atc acc gcc gac aag cag aag	477
	Asn Tyr Asn Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys	
	145 150 155	
30	Venus F1D, F64L,M153T mutations, Met @ pos. 1 removed	
	SEQ ID NOS:644 & 645	
35	gtg agc aag ggc gag gag ctg ttc acc ggc gtg gtg ccc atc ctg gtc	48
	Val Ser Lys Gly Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val	
	1 5 10 15	
40	gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag	96
	Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu	
	20 25 30	
45	ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc tgc	144
	Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys	
	35 40 45	
	acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ctg	192
	Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Leu	
	50 55 60	
50	ggc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag cgg	240
	Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg	
	65 70 75 80	
55	cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc	288
	His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg	
	85 90 95	



	acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag gtg	336
	Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val	
	100 105 110	
5	aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc atc	384
	Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile	
	115 120 125	
10	gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac	432
	Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn	
	130 135 140	
	tac aac agc cac aac gtc tat atc acc gcc gac aag cag aag	474
	Tyr Asn Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys	
15	145 150 155	
Venus F1D, F46L,M153T mutations		
20	SEQ ID NOS:646 & 647	
	atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg	48
	Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu	
	1 5 10 15	
25	gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc	96
	Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly	
	20 25 30	
30	gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ctg atc	144
	Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Leu Ile	
	35 40 45	
35	tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc	192
	Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr	
	50 55 60	
	ttc ggc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag	240
	Phe Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys	
40	65 70 75 80	
	cgg cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag	288
	Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu	
	85 90 95	
45	cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag	336
	Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu	
	100 105 110	
50	gtg aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc	384
	Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly	
	115 120 125	
55	atc gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac	432
	Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr	
	130 135 140	

aac tac aac agc cac aac gtc tat atc acc gcc gac aag cag aag 477  
Asn Tyr Asn Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys  
145 150 155

Venus F1D, F46L,M153T mutations, Met @ pos. 1 removed  
SEQ ID NOS:648 & 649

gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag 96  
Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu  
20 25 30

ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ctg atc tgc 144  
Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Leu Ile Cys  
35 40 45

acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ttc 192  
Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe  
50 55 60

ggc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag cgg 240  
Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg  
65 70 75 80

cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc 288  
 His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg  
 85 90 95

acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag gtg 336  
Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val  
100 105 110

aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc atc 384  
Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile  
115 120 125

gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac 432  
Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn  
130 135 140

tac aac agc cac aac gtc tat atc acc gcc gac aag cag aag 474  
Tyr Asn Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys  
145 150 155

Venus F1D, F46L,F64L,M153T mutations  
SEQ ID NOS:650 & 651

	gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc	96
	Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly	
	20 25 30	
5		
	gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ctg atc	144
	Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Leu Ile	
	35 40 45	
10		
	tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc	192
	Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr	
	50 55 60	
15		
	ctg ggc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag	240
	Leu Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys	
	65 70 75 80	
20		
	cgg cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag	288
	Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu	
	85 90 95	
25		
	cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag	336
	Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu	
	100 105 110	
30		
	gtg aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc	384
	Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly	
	115 120 125	
35		
	atc gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac	432
	Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr	
	130 135 140	
40		
	aac tac aac agc cac aac gtc tat atc acc gcc gac aag cag aag	477
	Asn Tyr Asn Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys	
	145 150 155	
45		
	Venus F1D, F46L,F64L,M153T mutations, Met @ pos. 1 removed	
	SEQ ID NOS:652 & 653	
50		
	gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc	48
	Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val	
	1 5 10 15	
55		
	gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag	96
	Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu	
	20 25 30	
60		
	ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ctg atc tgc	144
	Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Leu Ile Cys	
	35 40 45	
65		
	acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ctg	192
	Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Leu	
	50 55 60	

	ggc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag cgg	240								
	Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg									
	65 70 75 80									
5	cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc	288								
	His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg									
	85 90 95									
10	acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag gtg	336								
	Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val									
	100 105 110									
15	aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc atc	384								
	Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile									
	115 120 125									
20	gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac	432								
	Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn									
	130 135 140									
	tac aac agc cac aac gtc tat atc acc gcc gac aag cag aag	474								
	Tyr Asn Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys									
	145 150 155									
25	CFP F1D, F46L, F64L, N146I mutations									
	SEQ ID NOS:654 & 655									
30	atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg	48								
	Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu									
	1 5 10 15									
35	gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc	96								
	Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly									
	20 25 30									
40	gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ctg atc	144								
	Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Leu Ile									
	35 40 45									
45	tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc	192								
	Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr									
	50 55 60									
	ctg ggc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag	240								
	Leu Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys									
	65 70 75 80									
50	cgg cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag	288								
	Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu									
	85 90 95									
55	cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag	336								
	Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu									
	100 105 110									

	gtg aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc	384
	Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly	
	115 120 125	
5	atc gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac	432
	Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr	
	130 135 140	
10	aac tac atc agc cac aac gtc tat atc atg gcc gac aag cag aag	477
	Asn Tyr Ile Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys	
	145 150 155	
15	CFP F1D, F46L,F64L,N146I mutations, Met @ pos. 1 removed	
	SEQ ID NOS:656 & 657	
20	gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc	48
	Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val	
	1 5 10 15	
25	gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag	96
	Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu	
	20 25 30	
30	ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ctg atc tgc	144
	Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Leu Ile Cys	
	35 40 45	
35	acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ctg	192
	Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Leu	
	50 55 60	
40	ggc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag cgg	240
	Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg	
	65 70 75 80	
45	cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc	288
	His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg	
	85 90 95	
50	acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag gtg	336
	Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val	
	100 105 110	
55	aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc atc	384
	Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile	
	115 120 125	
60	gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac	432
	Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn	
	130 135 140	
65	tac atc agc cac aac gtc tat atc atg gcc gac aag cag aag	474
	Tyr Ile Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys	
	145 150 155	

CFP F1D, F64L, S65T, Y66W mutations  
SEQ ID NOS:658 & 659

5	atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu	48
	1 5 10 15	
10	gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly	96
	20 25 30	
15	gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile	144
	35 40 45	
20	tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr	192
	50 55 60	
25	ctg acc tgg ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag Leu Thr Trp Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys	240
	65 70 75 80	
30	cgg cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu	288
	85 90 95	
35	cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu	336
	100 105 110	
40	gtg aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly	384
	115 120 125	
45	atc gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr	432
	130 135 140	
50	aac tac aac agc cac aac gtc tat atc atg gcc gac aag cag aag Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys	477
	145 150 155	

CFP F1D, F64L, S65T, Y66W mutations, Met @ pos. 1 removed  
SEQ ID NOS:660 & 661

50	gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val	48
	1 5 10 15	
55	gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu	96
	20 25 30	

	ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc tgc	144
	Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys	
	35 40 45	
5	acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ctg	192
	Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Leu	
	50 55 60	
10	acc tgg ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag cgg	240
	Thr Trp Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg	
	65 70 75 80	
15	cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc	288
	His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg	
	85 90 95	
20	acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag gtg	336
	Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val	
	100 105 110	
25	aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc atc	384
	Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile	
	115 120 125	
30	gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac	432
	Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn	
	130 135 140	
35	tac aac agc cac aac gtc tat atc atg gcc gac aag cag aag	474
	Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys	
	145 150 155	
40	CFP F1D, Y66W mutation	
	SEQ ID NOS:662 & 663	
40	atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg	48
	Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu	
	1 5 10 15	
45	gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc	96
	Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly	
	20 25 30	
50	gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc	144
	Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile	
	35 40 45	
55	tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc	192
	Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr	
	50 55 60	
55	ttc ggc tgg ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag	240
	Phe Gly Trp Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys	
	65 70 75 80	

	cgg cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag	288
	Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu	
	85 90 95	
5	cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag	336
	Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu	
	100 105 110	
10	gtg aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc	384
	Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly	
	115 120 125	
15	atc gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac	432
	Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr	
	130 135 140	
20	aac tac aac agc cac aac gtc tat atc atg gcc gac aag cag aag	477
	Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys	
	145 150 155	
25	CFP F1D, Y66W mutation, Met @ pos. 1 removed	
	SEQ ID NOS:664 & 665	
30	gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc	48
	Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val	
	1 5 10 15	
35	gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag	96
	Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu	
	20 25 30	
40	ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc tgc	144
	Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys	
	35 40 45	
45	acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ttc	192
	Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe	
	50 55 60	
50	ggc tgg ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag cgg	240
	Gly Trp Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg	
	65 70 75 80	
55	cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc	288
	His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg	
	85 90 95	
60	acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag gtg	336
	Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val	
	100 105 110	
65	aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc atc	384
	Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile	
	115 120 125	



	gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac	432
	Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn	
	130 135 140	
5	tac aac agc cac aac gtc tat atc atg gcc gac aag cag aag	474
	Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys	
	145 150 155	
10		
	CFP F1D, Y66W,N146I mutations	
	SEQ ID NOS:666 & 667	
15	atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg	48
	Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu	
	1 5 10 15	
20	gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc	96
	Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly	
	20 25 30	
25	gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc	144
	Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile	
	35 40 45	
30	tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc	192
	Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr	
	50 55 60	
35	ttc ggc tgg ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag	240
	Phe Gly Trp Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys	
	65 70 75 80	
40	cgg cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag	288
	Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu	
	85 90 95	
45	cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag	336
	Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu	
	100 105 110	
50	gtg aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc	384
	Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly	
	115 120 125	
55	atc gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac	432
	Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr	
	130 135 140	
60	aac tac atc agc cac aac gtc tat atc atg gcc gac aag cag aag	477
	Asn Tyr Ile Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys	
	145 150 155	

CFP F1D, Y66W,N146I mutations, Met @ pos. 1 removed  
SEQ ID NOS:668 & 669

5	gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val	48
	1 5 10 15	
10	gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu	96
	20 25 30	
15	ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc tgc Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys	144
	35 40 45	
20	acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ttc Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe	192
	50 55 60	
25	ggc tgg ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag cgg Gly Trp Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg	240
	65 70 75 80	
30	cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg	288
	85 90 95	
35	acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag gtg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val	336
	100 105 110	
40	aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc atc Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile	384
	115 120 125	
45	gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn	432
	130 135 140	
50	tac atc agc cac aac gtc tat atc atg gcc gac aag cag aag Tyr Ile Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys	474
	145 150 155	

CFP F1D, Y66W,M153T mutations  
SEQ ID NOS:670 & 671

50	atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu	48
	1 5 10 15	
55	gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly	96
	20 25 30	

	gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc	144
	Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile	
	35 40 45	
5	tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc	192
	Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr	
	50 55 60	
10	ttc ggc tgg ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag	240
	Phe Gly Trp Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys	
	65 70 75 80	
15	cgg cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag	288
	Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu	
	85 90 95	
20	cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag	336
	Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu	
	100 105 110	
25	gtg aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc	384
	Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly	
	115 120 125	
30	atc gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac	432
	Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr	
	130 135 140	
35	aac tac aac agc cac aac gtc tat atc acc gcc gac aag cag aag	477
	Asn Tyr Asn Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys	
	145 150 155	
40	CFP F1D, Y66W,M153T mutations, Met @ pos. 1 removed	
	SEQ ID NOS:672 & 673	
45	gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc	48
	Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val	
	1 5 10 15	
50	gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag	96
	Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu	
	20 25 30	
55	ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc tgc	144
	Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys	
	35 40 45	
60	acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ttc	192
	Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe	
	50 55 60	
65	ggc tgg ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag cgg	240
	Gly Trp Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg	
	65 70 75 80	

	cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc	288
	His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg	
	85 90 95	
5	acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag gtg	336
	Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val	
	100 105 110	
10	aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc atc	384
	Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile	
	115 120 125	
15	gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac	432
	Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn	
	130 135 140	
20	tac aac agc cac aac gtc tat atc acc gcc gac aag cag aag	474
	Tyr Asn Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys	
	145 150 155	
	CFP F1D, N146I mutation	
	SEQ ID NOS:674 & 675	
25	atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg	48
	Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu	
	1 5 10 15	
30	gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc	96
	Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly	
	20 25 30	
35	gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc	144
	Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile	
	35 40 45	
40	tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc	192
	Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr	
	50 55 60	
45	ttc ggc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag	240
	Phe Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys	
	65 70 75 80	
	cgg cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag	288
	Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu	
	85 90 95	
50	cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag	336
	Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu	
	100 105 110	
55	gtg aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc	384
	Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly	
	115 120 125	

	atc gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac	432
	Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr	
	130 135 140	
5	aac tac atc agc cac aac gtc tat atc atg gcc gac aag cag aag	477
	Asn Tyr Ile Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys	
	145 150 155	
10		
	CFP F1D, N146I mutation, Met @ pos. 1 removed	
	SEQ ID NOS:676 & 677	
15	gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc	48
	Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val	
	1 5 10 15	
20	gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag	96
	Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu	
	20 25 30	
25	ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc tgc	144
	Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys	
	35 40 45	
30	acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ttc	192
	Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe	
	50 55 60	
35	ggc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag cgg	240
	Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg	
	65 70 75 80	
40	cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc	288
	His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg	
	85 90 95	
45	acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag gtg	336
	Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val	
	100 105 110	
50	aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc atc	384
	Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile	
	115 120 125	
55	gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac	432
	Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn	
	130 135 140	
60	tac atc agc cac aac gtc tat atc atg gcc gac aag cag aag	474
	Tyr Ile Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys	
	145 150 155	

CFP F1D, M153T mutation  
SEQ ID NOS:678 & 679

5	atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu	48
	1 5 10 15	
10	gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly	96
	20 25 30	
15	gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile	144
	35 40 45	
20	tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr	192
	50 55 60	
25	ttc ggc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag Phe Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys	240
	65 70 75 80	
30	cgg cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu	288
	85 90 95	
35	cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu	336
	100 105 110	
40	gtg aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly	384
	115 120 125	
45	atc gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr	432
	130 135 140	
50	aac tac aac agc cac aac gtc tat atc acc gcc gac aag cag aag Asn Tyr Asn Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys	477
	145 150 155	

CFP F1D, M153T mutation, Met @ pos. 1 removed  
SEQ ID NOS:680 & 681

50	gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val	48
	1 5 10 15	
55	gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu	96
	20 25 30	

	ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc tgc	144
	Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys	
	35 40 45	
5	acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ttc	192
	Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe	
	50 55 60	
10	ggc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag cgg	240
	Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg	
	65 70 75 80	
15	cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc	288
	His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg	
	85 90 95	
20	acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag gtg	336
	Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val	
	100 105 110	
25	aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc atc	384
	Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile	
	115 120 125	
30	gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac	432
	Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn	
	130 135 140	
35	tac aac agc cac aac gtc tat atc acc gcc gac aag cag aag	474
	Tyr Asn Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys	
	145 150 155	
40	atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg	48
	Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu	
	1 5 10 15	
45	gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc	96
	Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly	
	20 25 30	
50	gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc	144
	Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile	
	35 40 45	
55	tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc	192
	Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr	
	50 55 60	
60	ttc ggc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag	240
	Phe Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys	
	65 70 75 80	

CFP F1D, N146I,M153T mutations  
SEQ ID NOS:682 & 683

	cgg cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag	288
	Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu	
	85 90 95	
5	cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag	336
	Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu	
	100 105 110	
10	gtg aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc	384
	Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly	
	115 120 125	
15	atc gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac	432
	Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr	
	130 135 140	
20	aac tac atc agc cac aac gtc tat atc acc gcc gac aag cag aag	477
	Asn Tyr Ile Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys	
	145 150 155	
CFP F1D, N146I, M153T mutations, Met @ pos. 1 removed		
SEQ ID NOS:684 & 685		
25	gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc	48
	Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val	
	1 5 10 15	
30	gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag	96
	Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu	
	20 25 30	
35	ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc tgc	144
	Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys	
	35 40 45	
40	acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ttc	192
	Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe	
	50 55 60	
45	ggc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag cgg	240
	Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg	
	65 70 75 80	
50	cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc	288
	His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg	
	85 90 95	
55	acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag gtg	336
	Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val	
	100 105 110	
55	aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc atc	384
	Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile	
	115 120 125	



	gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac	432
	Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn	
	130 135 140	
5	tac atc agc cac aac gtc tat atc acc gcc gac aag cag aag	474
	Tyr Ile Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys	
	145 150 155	
10	CFP F1D, Y66W, N146I, M153T mutations SEQ ID NOS:686 & 687	
15	atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg	48
	Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu	
	1 5 10 15	
20	gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc	96
	Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly	
	20 25 30	
25	gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc	144
	Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile	
	35 40 45	
30	tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc	192
	Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr	
	50 55 60	
35	ttc ggc tgg ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag	240
	Phe Gly Trp Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys	
	65 70 75 80	
40	cgg cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag	288
	Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu	
	85 90 95	
45	cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag	336
	Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu	
	100 105 110	
50	gtg aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc	384
	Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly	
	115 120 125	
55	atc gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac	432
	Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr	
	130 135 140	
60	aac tac atc agc cac aac gtc tat atc acc gcc gac aag cag aag	477
	Asn Tyr Ile Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys	
	145 150 155	
65	CFP F1D, Y66W, N146I, M153T mutations, Met @ pos. 1 removed SEQ ID NOS:688 & 689	

	gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val 1 5 10 15	48														
5	gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu 20 25 30	96														
10	ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc tgc Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys 35 40 45	144														
15	acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ttc Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe 50 55 60	192														
20	ggc tgg ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag cgg Gly Trp Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg 65 70 75 80	240														
25	cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg 85 90 95	288														
30	acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag gtg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val 100 105 110	336														
35	aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc atc Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile 115 120 125	384														
40	gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn 130 135 140	432														
45	tac atc agc cac aac gtc tat atc acc gcc gac aag cag aag Tyr Ile Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys 145 150 155	474														
50	CFP F1D, S65A mutation SEQ ID NOS:690 & 691															
55	atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu 1 5 10 15	48														
60	gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly 20 25 30	96														
65	gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile 35 40 45	144														

	tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc	192
	Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr	
	50 55 60	
5	ttc gcc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag	240
	Phe Ala Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys	
	65 70 75 80	
10	cgg cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag	288
	Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu	
	85 90 95	
15	cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag	336
	Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu	
	100 105 110	
20	gtg aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc	384
	Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly	
	115 120 125	
25	atc gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac	432
	Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr	
	130 135 140	
30	aac tac aac agc cac aac gtc tat atc atg gcc gac aag cag aag	477
	Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys	
	145 150 155	
35	CFP F1D, S65A mutation, Met @ pos. 1 removed	
	SEQ ID NOS:692 & 693	
40	gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc	48
	Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val	
	1 5 10 15	
45	gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag	96
	Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu	
	20 25 30	
50	ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc tgc	144
	Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys	
	35 40 45	
55	acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ttc	192
	Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe	
	50 55 60	
60	gcc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag cgg	240
	Ala Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg	
	65 70 75 80	
65	cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc	288
	His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg	
	85 90 95	

	acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag gtg	336
	Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val	
	100 105 110	
5	aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc atc	384
	Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile	
	115 120 125	
10	gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac	432
	Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn	
	130 135 140	
15	tac aac agc cac aac gtc tat atc atg gcc gac aag cag aag	474
	Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys	
	145 150 155	
20	CFP F1D, S65A,Y66W,S72A mutations SEQ ID NOS:694 & 695	
25	atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg	48
	Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu	
	1 5 10 15	
30	gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc	96
	Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly	
	20 25 30	
35	gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc	144
	Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile	
	35 40 45	
40	tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc	192
	Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr	
	50 55 60	
45	ttc gcc tgg ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag	240
	Phe Ala Trp Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys	
	65 70 75 80	
50	cgg cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag	288
	Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu	
	85 90 95	
55	cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag	336
	Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu	
	100 105 110	
60	gtg aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc	384
	Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly	
	115 120 125	
65	atc gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac	432
	Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr	
	130 135 140	

aac tac aac agc cac aac gtc tat atc atg gcc gac aag cag aag 477  
Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys  
145 150 155

5

gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc      48  
10 Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val  
                5                         10                         15

gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag 96  
Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu  
15 20 25 30

ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc tgc 144  
Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys  
35 40 45

acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ttc 192  
Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe  
50 55 60

25 gcc tgg ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag cgg 240  
Ala Trp Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg  
65 70 75 80

30      cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc      288  
His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg  
                85                         90                         95

acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag gtg 336  
Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val  
35 100 105 110

aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc atc 384  
Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile  
115 120 125

gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac 432  
Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn  
130 135 140

45    tac aac agc cac aac gtc tat atc atg gcc gac aag cag aag                      474  
Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys  
145                          150                          155

50

55     atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg                48  
     Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu  
     1                      5                      ~                      10                      15

	gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc	96
	Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly	
	20 25 30	
5	gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc	144
	Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile	
	35 40 45	
10	tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc	192
	Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr	
	50 55 60	
15	ttc ggc cac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag	240
	Phe Gly His Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys	
	65 70 75 80	
20	cgg cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag	288
	Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu	
	85 90 95	
25	cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag	336
	Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu	
	100 105 110	
30	gtg aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc	384
	Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly	
	115 120 125	
35	atc gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac	432
	Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr	
	130 135 140	
40	aac tac aac agc cac aac gtc tat atc atg gcc gac aag cag aag	477
	Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys	
	145 150 155	
40	BFP F1D, Y66H mutation, Met @ pos. 1 removed	
	SEQ ID NOS:700 & 701	
45	gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc	48
	Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val	
	1 5 10 15	
50	gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag	96
	Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu	
	20 25 30	
55	ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc tgc	144
	Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys	
	35 40 45	
55	acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ttc	192
	Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe	
	50 55 60	

	ggc cac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag cgg	240
	Gly His Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg	
	65 70 75 80	
5	cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc	288
	His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg	
	85 90 95	
10	acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag gtg	336
	Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val	
	100 105 110	
15	aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc atc	384
	Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile	
	115 120 125	
20	gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac	432
	Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn	
	130 135 140	
25	tac aac agc cac aac gtc tat atc atg gcc gac aag cag aag	474
	Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys	
	145 150 155	
	BFP F1D, F64L,Y66H mutations	
	SEQ ID NOS:702 & 703	
30	atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg	48
	Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu	
	1 5 10 15	
35	gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc	96
	Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly	
	20 25 30	
40	gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc	144
	Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile	
	35 40 45	
45	tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc	192
	Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr	
	50 55 60	
50	ctc ggc cac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag	240
	Leu Gly His Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys	
	65 70 75 80	
55	cgg cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag	288
	Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu	
	85 90 95	
55	cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag	336
	Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu	
	100 105 110	

	gtg aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc	384
	Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly	
	115 120 125	
5	atc gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac	432
	Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr	
	130 135 140	
10	aac tac aac agc cac aac gtc tat atc atg gcc gac aag cag aag	477
	Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys	
	145 150 155	
15	BFP F1D, F64L,Y66H mutations, Met @ pos. 1 removed	
	SEQ ID NOS:704 & 705	
20	gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc	48
	Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val	
	1 5 10 15	
25	gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag	96
	Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu	
	20 25 30	
30	ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc tgc	144
	Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys	
	35 40 45	
35	acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ctc	192
	Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Leu	
	50 55 60	
40	ggc cac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag cgg	240
	Gly His Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg	
	65 70 75 80	
45	cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc	288
	His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg	
	85 90 95	
50	acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag gtg	336
	Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val	
	100 105 110	
55	aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc atc	384
	Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile	
	115 120 125	
60	gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac	432
	Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn	
	130 135 140	
65	tac aac agc cac aac gtc tat atc atg gcc gac aag cag aag	474
	Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys	
	145 150 155	



BFP F1D, F64L,Y66H, Y145F mutations  
SEQ ID NOS:706 & 707

5	atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu 1 5 10 15	48
10	gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly 20 25 30	96
15	gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile 35 40 45	144
20	tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr 50 55 60	192
25	ctc ggc cac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag Leu Gly His Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys 65 70 75 80	240
30	cgg cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu 85 90 95	288
35	cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu 100 105 110	336
40	gtg aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly 115 120 125	384
45	atc gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr 130 135 140	432
50	aac ttc aac agc cac aac gtc tat atc atg gcc gac aag cag aag Asn Phe Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys 145 150 155	477

BFP F1D, F64L,Y66H,Y145F mutations, Met @ pos. 1 removed  
SEQ ID NOS:708 & 709

50	gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val 1 5 10 15	48
55	gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu 20 25 30	96

	ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc tgc	144
	Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys	
	35 40 45	
5	acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ctc	192
	Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Leu	
	50 55 60	
10	ggc cac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag cgg	240
	Gly His Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg	
	65 70 75 80	
15	cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc	288
	His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg	
	85 90 95	
20	acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag gtg	336
	Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val	
	100 105 110	
25	aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc atc	384
	Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile	
	115 120 125	
30	gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac	432
	Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn	
	130 135 140	
35	ttc aac agc cac aac gtc tat atc atg gcc gac aag cag aag	474
	Phe Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys	
	145 150 155	
40	BFP F1D, Y145F mutation	
	SEQ ID NOS:710 & 711	
45	atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg	48
	Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu	
	1 5 10 15	
50	gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc	96
	Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly	
	20 25 30	
55	gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc	144
	Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile	
	35 40 45	
60	tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc	192
	Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr	
	50 55 60	
65	ttc ggc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag	240
	Phe Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys	
	65 70 75 80	

	cgg	cac	gac	ttc	ttc	aag	tcc	gcc	atg	ccc	gaa	ggc	tac	gtc	cag	gag	288
	Arg	His	Asp	Phe	Phe	Lys	Ser	Ala	Met	Pro	Glu	Gly	Tyr	Val	Gln	Glu	
				85						90					95		
5	cgc	acc	atc	ttc	ttc	aag	gac	gac	ggc	aac	tac	aag	acc	cgc	gcc	gag	336
	Arg	Thr	Ile	Phe	Phe	Lys	Asp	Asp	Gly	Asn	Tyr	Lys	Thr	Arg	Ala	Glu	
				100					105					110			
10	gtg	aag	ttc	gag	ggc	gac	acc	ctg	gtg	aac	cgc	atc	gag	ctg	aag	ggc	384
	Val	Lys	Phe	Glu	Gly	Asp	Thr	Leu	Val	Asn	Arg	Ile	Glu	Leu	Lys	Gly	
				115				120					125				
15	atc	gac	ttc	aag	gag	gac	ggc	aac	atc	ctg	ggg	cac	aag	ctg	gag	tac	432
	Ile	Asp	Phe	Lys	Glu	Asp	Gly	Asn	Ile	Leu	Gly	His	Lys	Leu	Glu	Tyr	
		130					135					140					
20	aac	ttc	aac	agc	cac	aac	gtc	tat	atc	atg	gcc	gac	aag	cag	aag		477
	Asn	Phe	Asn	Ser	His	Asn	Val	Tyr	Ile	Met	Ala	Asp	Lys	Gln	Lys		
		145				150					155						
25	BFP F1D, Y145F mutation, Met @ pos. 1 removed SEQ ID NOS:712 & 713																
30	gtg	agc	aag	ggc	gag	gag	ctg	ttc	acc	ggg	gtg	gtg	ccc	atc	ctg	gtc	48
	Val	Ser	Lys	Gly	Glu	Glu	Leu	Phe	Thr	Gly	Val	Val	Pro	Ile	Leu	Val	
	1				5					10					15		
35	gag	ctg	gac	ggc	gac	gta	aac	ggc	cac	aag	ttc	agc	gtg	tcc	ggc	gag	96
	Glu	Leu	Asp	Gly	Asp	Val	Asn	Gly	His	Lys	Phe	Ser	Val	Ser	Gly	Glu	
				20				25						30			
40	ggc	gag	ggc	gat	gcc	acc	tac	ggc	aag	ctg	acc	ctg	aag	ttc	atc	tgc	144
	Gly	Glu	Gly	Asp	Ala	Thr	Tyr	Gly	Lys	Leu	Thr	Leu	Lys	Phe	Ile	Cys	
			35					40					45				
45	acc	acc	ggc	aag	ctg	ccc	gtg	ccc	tgg	ccc	acc	ctc	gtg	acc	acc	ttc	192
	Thr	Thr	Gly	Lys	Leu	Pro	Val	Pro	Trp	Pro	Thr	Leu	Val	Thr	Thr	Phe	
			50				55					60					
50	ggc	tac	ggc	ctg	cag	tgc	ttc	gcc	cgc	tac	ccc	gac	cac	atg	aag	cgg	240
	Gly	Tyr	Gly	Leu	Gln	Cys	Phe	Ala	Arg	Tyr	Pro	Asp	His	Met	Lys	Arg	
	65				70					75					80		
55	cac	gac	ttc	ttc	aag	tcc	gcc	atg	ccc	gaa	ggc	tac	gtc	cag	gag	cgc	288
	His	Asp	Phe	Phe	Lys	Ser	Ala	Met	Pro	Glu	Gly	Tyr	Val	Gln	Glu	Arg	
				85						90					95		
60	acc	atc	ttc	ttc	aag	gac	gac	ggc	aac	tac	aag	acc	cgc	gcc	gag	gtg	336
	Thr	Ile	Phe	Phe	Lys	Asp	Asp	Gly	Asn	Tyr	Lys	Thr	Arg	Ala	Glu	Val	
				100				105									

gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac 432  
 Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn  
 130 135 140

5

ttc aac agc cac aac gtc tat atc atg gcc gac aag cag aag 474  
 Phe Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys  
 145 150 155

10

BFP F1D, F46L,F64L,Y145F mutations  
 SEQ ID NOS:714 & 715

15

atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg 48  
 Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu  
 1 5 10 15

20

gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc 96  
 Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly  
 20 25 30

25

gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ctg atc 144  
 Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Leu Ile  
 35 40 45

30

tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc 192  
 Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr  
 50 55 60

35

ctg ggc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag 240  
 Leu Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys  
 65 70 75 80

40

cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag 288  
 Arg His Asp Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu  
 85 90 95

45

cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag 336  
 Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu  
 100 105 110

50

gtg aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc 384  
 Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly  
 115 120 125

55

atc gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac 432  
 Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr  
 130 135 140

aac ttc aac agc cac aac gtc tat atc atg gcc gac aag cag aag 477  
 Asn Phe Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys  
 145 150 155

BFP F1D, F46L,F64L,Y145F mutations, Met @ pos. 1 removed  
 SEQ ID NOS:716 & 717

5	gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val 1 5 10 15	48
10	gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu 20 25 30	96
15	ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ctg atc tgc Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Leu Ile Cys 35 40 45	144
20	acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ctg Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Leu 50 55 60	192
25	ggc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag cgg Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg 65 70 75 80	240
30	cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg 85 90 95	288
35	acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag gtg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val 100 105 110	336
40	aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc atc Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile 115 120 125	384
45	gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn 130 135 140	432
50	ttc aac agc cac aac gtc tat atc atg gcc gac aag cag aag Phe Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys 145 150 155	474

YFP F2D, Met added @ pos. 1  
 (YFP F2D corresponds to aa residues 159-239 of YFP)  
 SEQ ID NOS:718 & 719

50	atg aac ggc atc aag gtg aac ttc aag atc cgc cac aac atc gag gac Met Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp 1 5 10 15	48
55	ggc agc gtg cag ctc gcc gac cac tac cag cag aac acc ccc atc ggc Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly 20 25 30	96

	gac ggc ccc gtg ctg ctg ccc gac aac cac tac ctg agc tac cag tcc	144
	Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Tyr Gln Ser	
	35 40 45	
5	gcc ctg agc aaa gac ccc aac gag aag cgc gat cac atg gtc ctg ctg	192
	Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu	
	50 55 60	
10	gag ttc gtg acc gcc gcc ggg atc act ctc ggc atg gac gag ctg tac	240
	Glu Phe Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr	
	65 70 75 80	
	aag	243
	Lys	
15		
	YFP F2D, Y203F mutation	
	SEQ ID NOS:720 & 721	
20	aac ggc atc aag gtg aac ttc aag atc cgc cac aac atc gag gac ggc	48
	Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly	
	1 5 10 15	
25	agc gtg cag ctc gcc gac cac tac cag cag aac acc ccc atc ggc gac	96
	Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp	
	20 25 30	
30	ggc ccc gtg ctg ctg ccc gac aac cac tac ctg agc tac cag tcc gcc	144
	Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Tyr Gln Ser Ala	
	35 40 45	
35	ctg agc aaa gac ccc aac gag aag cgc gat cac atg gtc ctg ctg gag	192
	Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu	
	50 55 60	
40	ttc gtg acc gcc gcc ggg atc act ctc ggc atg gac gag ctg tac aag	240
	Phe Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys	
	65 70 75 80	
40	YFP F2D, Y203F mutation, Met added @ pos. 1	
	SEQ ID NOS:722 & 723	
45	atg aac ggc atc aag gtg aac ttc aag atc cgc cac aac atc gag gac	48
	Met Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp	
	1 5 10 15	
50	ggc agc gtg cag ctc gcc gac cac tac cag cag aac acc ccc atc ggc	96
	Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly	
	20 25 30	
55	gac ggc ccc gtg ctg ctg ccc gac aac cac tac ctg agc tac cag tcc	144
	Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Tyr Gln Ser	
	35 40 45	
55	gcc ctg agc aaa gac ccc aac gag aag cgc gat cac atg gtc ctg ctg	192
	Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu	
	50 55 60	

	gag	ttc	gtg	acc	gcc	gcc	ggg	atc	act	ctc	ggc	atg	gac	gag	ctg	tac	240
	Glu	Phe	Val	Thr	Ala	Ala	Gly	Ile	Thr	Leu	Gly	Met	Asp	Glu	Leu	Tyr	
	65					70					75					80	
5	aag																243
	Lys																
10	YFP F2D, Y203H mutation																
	SEQ ID NOS:724 & 725																
	aac	ggc	atc	aag	gtg	aac	ttc	aag	atc	cgc	cac	aac	atc	gag	gac	ggc	48
15	Asn	Gly	Ile	Lys	Val	Asn	Phe	Lys	Ile	Arg	His	Asn	Ile	Glu	Asp	Gly	
	1				5					10					15		
	agc	gtg	cag	ctc	gcc	gac	cac	tac	cag	cag	aac	acc	ccc	atc	ggc	gac	96
20	Ser	Val	Gln	Leu	Ala	Asp	His	Tyr	Gln	Gln	Asn	Thr	Pro	Ile	Gly	Asp	
				20					25					30			
	ggc	ccc	gtg	ctg	ctg	ccc	gac	aac	cac	tac	ctg	agc	cac	cag	tcc	gcc	144
25	Gly	Pro	Val	Leu	Leu	Pro	Asp	Asn	His	Tyr	Leu	Ser	His	Gln	Ser	Ala	
			35					40					45				
	ctg	agc	aaa	gac	ccc	aac	gag	aag	cgc	gat	cac	atg	gtc	ctg	ctg	gag	192
	Leu	Ser	Lys	Asp	Pro	Asn	Glu	Lys	Arg	Asp	His	Met	Val	Leu	Leu	Glu	
		50					55					60					
30	ttc	gtg	acc	gcc	gcc	ggg	atc	act	ctc	ggc	atg	gac	gag	ctg	tac	aag	240
	Phe	Val	Thr	Ala	Ala	Gly	Ile	Thr	Leu	Gly	Met	Asp	Glu	Leu	Tyr	Lys	
	65					70					75					80	
35	YFP F2D, Y203H mutation, Met added @ pos. 1																
	SEQ ID NOS:726 & 727																
	atg	aac	ggc	atc	aag	gtg	aac	ttc	aag	atc	cgc	cac	aac	atc	gag	gac	48
40	Met	Asn	Gly	Ile	Lys	Val	Asn	Phe	Lys	Ile	Arg	His	Asn	Ile	Glu	Asp	
	1				5					10					15		
	ggc	agc	gtg	cag	ctc	gcc	gac	cac	tac	cag	cag	aac	acc	ccc	atc	ggc	96
	Gly	Ser	Val	Gln	Leu	Ala	Asp	His	Tyr	Gln	Gln	Asn	Thr	Pro	Ile	Gly	
				20					25					30			
45	gac	ggc	ccc	gtg	ctg	ctg	ccc	gac	aac	cac	tac	ctg	agc	cac	cag	tcc	144
	Asp	Gly	Pro	Val	Leu	Leu	Pro	Asp	Asn	His	Tyr	Leu	Ser	His	Gln	Ser	
			35					40					45				
50	gcc	ctg	agc	aaa	gac	ccc	aac	gag	aag	cgc	gat	cac	atg	gtc	ctg	ctg	192
	Ala	Leu	Ser	Lys	Asp	Pro	Asn	Glu	Lys	Arg	Asp	His	Met	Val	Leu	Leu	
		50					55					60					
55	gag	ttc	gtg	acc	gcc	gcc	ggg	atc	act	ctc	ggc	atg	gac	gag	ctg	tac	240
	Glu	Phe	Val	Thr	Ala	Ala	Gly	Ile	Thr	Leu	Gly	Met	Asp	Glu	Leu	Tyr	
	65					70					75					80	

	aag		243
	Lys		
5	CFP F2D, Y203T mutation SEQ ID NOS:728 & 729		
10	aac ggc atc aag gtg aac ttc aag atc cgc cac aac atc gag gac ggc Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly	48	
	1 5 10 15		
15	agc gtg cag ctc gcc gac cac tac cag cag aac acc ccc atc ggc gac Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp	96	
	20 25 30		
20	ggc ccc gtg ctg ctg ccc gac aac cac tac ctg agc acc cag tcc gcc Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala	144	
	35 40 45		
25	ctg agc aaa gac ccc aac gag aag cgc gat cac atg gtc ctg ctg gag Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu	192	
	50 55 60		
30	ttc gtg acc gcc gcc ggg atc act ctc ggc atg gac gag ctg tac aag Phe Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys	240	
	65 70 75 80		
30	CFP F2D, Y203T mutation, Met added @ pos. 1 SEQ ID NOS:730 & 731		
35	atg aac ggc atc aag gtg aac ttc aag atc cgc cac aac atc gag gac Met Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp	48	
	1 5 10 15		
40	ggc agc gtg cag ctc gcc gac cac tac cag cag aac acc ccc atc ggc Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly	96	
	20 25 30		
45	gac ggc ccc gtg ctg ctg ccc gac aac cac tac ctg agc acc cag tcc Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser	144	
	35 40 45		
50	gcc ctg agc aaa gac ccc aac gag aag cgc gat cac atg gtc ctg ctg Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu	192	
	50 55 60		
55	gag ttc gtg acc gcc gcc ggg atc act ctc ggc atg gac gag ctg tac Glu Phe Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr	240	
	65 70 75 80		
	aag	243	
	Lys		



CFP F2D, V163A,Y203T mutations  
SEQ ID NOS:732 & 733

5	aac ggc atc aag gcc aac ttc aag atc cgc cac aac atc gag gac ggc Asn Gly Ile Lys Ala Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly 1 5 10 15	48
10	agc gtg cag ctc gcc gac cac tac cag cag aac acc ccc atc ggc gac Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp 20 25 30	96
15	ggc ccc gtg ctg ctg ccc gac aac cac tac ctg agc acc cag tcc gcc Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala 35 40 45	144
20	ctg agc aaa gac ccc aac gag aag cgc gat cac atg gtc ctg ctg gag Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu 50 55 60	192
25	ttc gtg acc gcc gcc ggg atc act ctc ggc atg gac gag ctg tac aag Phe Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys 65 70 75 80	240

CFP F2D, V163A,Y203T, Met added @ pos. 1  
SEQ ID NOS:734 & 735

30	atg aac ggc atc aag gcc aac ttc aag atc cgc cac aac atc gag gac Met Asn Gly Ile Lys Ala Asn Phe Lys Ile Arg His Asn Ile Glu Asp 1 5 10 15	48
35	ggc agc gtg cag ctc gcc gac cac tac cag cag aac acc ccc atc ggc Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly 20 25 30	96
40	gac ggc ccc gtg ctg ctg ccc gac aac cac tac ctg agc acc cag tcc Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser 35 40 45	144
45	gcc ctg agc aaa gac ccc aac gag aag cgc gat cac atg gtc ctg ctg Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu 50 55 60	192
50	gag ttc gtg acc gcc gcc ggg atc act ctc ggc atg gac gag ctg tac Glu Phe Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr 65 70 75 80	240
55	aag Lys	243

Venus F2D, S175G mutation  
SEQ ID NOS:736 & 737

5	aac ggc atc aag gtg aac ttc aag atc cgc cac aac atc gag gac ggc Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly 1 5 10 15	48
10	ggc gtg cag ctc gcc gac cac tac cag cag aac acc ccc atc ggc gac Gly Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp 20 25 30	96
15	ggc ccc gtg ctg ctg ccc gac aac cac tac ctg agc tac cag tcc gcc Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Tyr Gln Ser Ala 35 40 45	144
20	ctg agc aaa gac ccc aac gag aag cgc gat cac atg gtc ctg ctg gag Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu 50 55 60	192
25	ttc gtg acc gcc gcc ggg atc act ctc ggc atg gac gag ctg tac aag Phe Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys 65 70 75 80	240

25 Venus F2D, S175G mutation, Met added @ pos. 1  
SEQ ID NOS:738 & 739

30	atg aac ggc atc aag gtg aac ttc aag atc cgc cac aac atc gag gac Met Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp 1 5 10 15	48
35	ggc ggc gtg cag ctc gcc gac cac tac cag cag aac acc ccc atc ggc Gly Gly Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly 20 25 30	96
40	gac ggc ccc gtg ctg ctg ccc gac aac cac tac ctg agc tac cag tcc Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Tyr Gln Ser 35 40 45	144
45	gcc ctg agc aaa gac ccc aac gag aag cgc gat cac atg gtc ctg ctg Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu 50 55 60	192
50	gag ttc gtg acc gcc gcc ggg atc act ctc ggc atg gac gag ctg tac Glu Phe Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr 65 70 75 80	240

50	aag Lys	243
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Venus F2D, V163A,S175G mutations  
SEQ ID NOS:740 & 741

55	aac ggc atc aag gcc aac ttc aag atc cgc cac aac atc gag gac ggc Asn Gly Ile Lys Ala Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly 1 5 10 15	48
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	ggc gtg cag ctc gcc gac cac tac cag cag aac acc ccc atc ggc gac	96
	Gly Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp	
	20 25 30	
5	ggc ccc gtg ctg ctg ccc gac aac cac tac ctg agc tac cag tcc gcc	144
	Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Tyr Gln Ser Ala	
	35 40 45	
10	ctg agc aaa gac ccc aac gag aag cgc gat cac atg gtc ctg ctg gag	192
	Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu	
	50 55 60	
15	ttc gtg acc gcc gcc ggg atc act ctc ggc atg gac gag ctg tac aag	240
	Phe Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys	
	65 70 75 80	
20	Venus F2D, V163A,S175G, Met added @ pos. 1	
	SEQ ID NOS:742 & 743	
	atg aac ggc atc aag gcc aac ttc aag atc cgc cac aac atc gag gac	48
	Met Asn Gly Ile Lys Ala Asn Phe Lys Ile Arg His Asn Ile Glu Asp	
	1 5 10 15	
25	ggc ggc gtg cag ctc gcc gac cac tac cag cag aac acc ccc atc ggc	96
	Gly Gly Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly	
	20 25 30	
30	gac ggc ccc gtg ctg ctg ccc gac aac cac tac ctg agc tac cag tcc	144
	Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Tyr Gln Ser	
	35 40 45	
35	gcc ctg agc aaa gac ccc aac gag aag cgc gat cac atg gtc ctg ctg	192
	Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu	
	50 55 60	
40	gag ttc gtg acc gcc gcc ggg atc act ctc ggc atg gac gag ctg tac	240
	Glu Phe Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr	
	65 70 75 80	
	aag	243
	Lys	
45		
	YFP F1E, pos. 1 Met removed	
	(YFP F1E corresponds to aa residues 1-174 of YFP)	
	SEQ ID NOS:744 & 745	
50	gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc	48
	Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val	
	1 5 10 15	
55	gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag	96
	Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu	
	20 25 30	

	ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc tgc	144
	Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys	
	35 40 45	
5	acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ttc	192
	Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe	
	50 55 60	
10	ggc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag cgg	240
	Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg	
	65 70 75 80	
15	cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc	288
	His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg	
	85 90 95	
20	acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag gtg	336
	Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val	
	100 105 110	
25	aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc atc	384
	Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile	
	115 120 125	
30	gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac	432
	Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn	
	130 135 140	
35	tac aac agc cac aac gtc tat atc atg gcc gac aag cag aag aac ggc	480
	Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly	
	145 150 155 160	
40	atc aag gtg aac ttc aag atc cgc cac aac atc gag gac	519
	Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp	
	165 170	
40	YFP F1E, K79R mutation	
	SEQ ID NOS:746 & 747	
45	atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg	48
	Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu	
	1 5 10 15	
50	gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc	96
	Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly	
	20 25 30	
55	gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc	144
	Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile	
	35 40 45	
55	tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc	192
	Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr	
	50 55 60	

	ttc ggc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg cgc	240
	Phe Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Arg	
	65 70 75 80	
5	cgg cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag	288
	Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu	
	85 90 95	
10	cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag	336
	Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu	
	100 105 110	
15	gtg aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc	384
	Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly	
	115 120 125	
20	atc gac ttc aag gag gac ggc aac atc ctg ggc cac aag ctg gag tac	432
	Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr	
	130 135 140	
25	aac tac aac agc cac aac gtc tat atc atg gcc gac aag cag aag aac	480
	Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn	
	145 150 155 160	
30	ggc atc aag gtg aac ttc aag atc cgc cac aac atc gag gac	522
	Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp	
	165 170	
30	YFP F1E, K79R mutation, pos. 1 Met removed	
	SEQ ID NOS:748 & 749	
35	gtg agc aag ggc gag gag ctg ttc acc ggc gtg gtg ccc atc ctg gtc	48
	Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val	
	1 5 10 15	
40	gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag	96
	Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu	
	20 25 30	
45	ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc tgc	144
	Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys	
	35 40 45	
50	acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ttc	192
	Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe	
	50 55 60	
55	ggc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg cgc cgg	240
	Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Arg Arg	
	65 70 75 80	
55	cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc	288
	His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg	
	85 90 95	

	acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag gtg	336
	Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val	
	100 105 110	
5	aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc atc	384
	Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile	
	115 120 125	
10	gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac	432
	Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn	
	130 135 140	
15	tac aac agc cac aac gtc tat atc atg gcc gac aag cag aag aac ggc	480
	Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly	
	145 150 155 160	
20	atc aag gtg aac ttc aag atc cgc cac aac atc gag gac	519
	Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp	
	165 170	
	YFP F1E, Y66F mutation	
	SEQ ID NOS:750 & 751	
25	atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg	48
	Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu	
	1 5 10 15	
30	gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc	96
	Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly	
	20 25 30	
35	gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc	144
	Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile	
	35 40 45	
40	tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc	192
	Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr	
	50 55 60	
45	ttc ggc ttc ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag	240
	Phe Gly Phe Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys	
	65 70 75 80	
50	cgg cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag	288
	Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu	
	85 90 95	
55	cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag	336
	Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu	
	100 105 110	
55	gtg aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc	384
	Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly	
	115 120 125	

	atc gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac	432
	Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr	
	130 135 140	
5	aac tac aac agc cac aac gtc tat atc atg gcc gac aag cag aag aac	480
	Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn	
	145 150 155 160	
10	ggc atc aag gtg aac ttc aag atc cgc cac aac atc gag gac	522
	Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp	
	165 170	
15	YFP F1E, Y66F mutation, pos. 1 Met removed SEQ ID NOS:752 & 753	
20	gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc	48
	Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val	
	1 5 10 15	
25	gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag	96
	Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu	
	20 25 30	
30	ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc tgc	144
	Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys	
	35 40 45	
35	acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ttc	192
	Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe	
	50 55 60	
40	ggc ttc ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag cgg	240
	Gly Phe Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg	
	65 70 75 80	
45	cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc	288
	His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg	
	85 90 95	
50	acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag gtg	336
	Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val	
	100 105 110	
55	aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc atc	384
	Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile	
	115 120 125	
60	gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac	432
	Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn	
	130 135 140	
65	tac aac agc cac aac gtc tat atc atg gcc gac aag cag aag aac ggc	480
	Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly	
	145 150 155 160	

atc aag gtg aac ttc aag atc cgc cac aac atc gag gac	519
Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp	
165 170	

5

YFP F1E, Q69K mutation  
SEQ ID NOS:754 & 755

10	atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg	48
	Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu	
	1 5 10 15	

15	gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc	96
	Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly	
	20 25 30	

20	gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc	144
	Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile	
	35 40 45	

25	tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc	192
	Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr	
	50 55 60	

30	ttc ggc tac ggc ctg aag tgc ttc gcc cgc tac ccc gac cac atg aag	240
	Phe Gly Tyr Gly Leu Lys Cys Phe Ala Arg Tyr Pro Asp His Met Lys	
	65 70 75 80	

35	cgg cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag	288
	Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu	
	85 90 95	

40	cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag	336
	Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu	
	100 105 110	

45	gtg aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc	384
	Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly	
	115 120 125	

50	atc gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac	432
	Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr	
	130 135 140	

55	aac tac aac agc cac aac gtc tat atc atg gcc gac aag cag aag aac	480
	Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn	
	145 150 155 160	

60	ggc atc aag gtg aac ttc aag atc cgc cac aac atc gag gac	522
	Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp	
	165 170	

55



YFP FlE, Q69K mutation, pos. 1 Met removed  
SEQ ID NOS:756 & 757

5	gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val 1 5 10 15	48
10	gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu 20 25 30	96
15	ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc tgc Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys 35 40 45	144
	acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ttc Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe 50 55 60	192
20	ggc tac ggc ctg aag tgc ttc gcc cgc tac ccc gac cac atg aag cgg Gly Tyr Gly Leu Lys Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg 65 70 75 80	240
25	cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg 85 90 95	288
30	acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag gtg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val 100 105 110	336
35	aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc atc Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile 115 120 125	384
	gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn 130 135 140	432
40	tac aac agc cac aac gtc tat atc atg gcc gac aag cag aag aac ggc Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly 145 150 155 160	480
45	atc aag gtg aac ttc aag atc cgc cac aac atc gag gac Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp 165 170	519

50  
citrine FlE, V68L,Q69M mutations  
SEQ ID NOS:758 & 759

55	atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu 1 5 10 15	48
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	gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc	96
	Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly	
	20 25 30	
5	gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc	144
	Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile	
	35 40 45	
10	tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc	192
	Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr	
	50 55 60	
15	ttc ggc tac ggc ctg atg tgc ttc gcc cgc tac ccc gac cac atg aag	240
	Phe Gly Tyr Gly Leu Met Cys Phe Ala Arg Tyr Pro Asp His Met Lys	
	65 70 75 80	
20	cgg cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag	288
	Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu	
	85 90 95	
25	cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag	336
	Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu	
	100 105 110	
30	gtg aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc	384
	Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly	
	115 120 125	
35	atc gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac	432
	Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr	
	130 135 140	
40	aac tac aac agc cac aac gtc tat atc atg gcc gac aag cag aag aac	480
	Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn	
	145 150 155 160	
45	ggc atc aag gtg aac ttc aag atc cgc cac aac atc gag gac	522
	Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp	
	165 170	
	citrine F1E,V68L,Q69M mutations, pos. 1 Met removed	
	SEQ ID NOS:760 & 761	
50	gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc	48
	Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val	
	1 5 10 15	
55	gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag	96
	Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu	
	20 25 30	
60	ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc tgc	144
	Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys	
	35 40 45	

	acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ttc	192
	Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe	
	50 55 60	
5	ggc tac ggc ctg atg tgc ttc gcc cgc tac ccc gac cac atg aag cgg	240
	Gly Tyr Gly Leu Met Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg	
	65 70 75 80	
10	cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc	288
	His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg	
	85 90 95	
15	acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag gtg	336
	Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val	
	100 105 110	
20	aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc atc	384
	Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile	
	115 120 125	
25	gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac	432
	Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn	
	130 135 140	
30	tac aac agc cac aac gtc tat atc atg gcc gac aag cag aag aac ggc	480
	Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly	
	145 150 155 160	
35	atc aag gtg aac ttc aag atc cgc cac aac atc gag gac	519
	Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp	
	165 170	
40	CFP F1E, F64L mutation	
	SEQ ID NOS:762 & 763	
45	atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg	48
	Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu	
	1 5 10 15	
50	gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc	96
	Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly	
	20 25 30	
55	gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc	144
	Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile	
	35 40 45	
60	tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc	192
	Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr	
	50 55 60	
65	ctg ggc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag	240
	Leu Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys	
	65 70 75 80	

	cgg	cac	gac	ttc	ttc	aag	tcc	gcc	atg	ccc	gaa	ggc	tac	gtc	cag	gag	288
	Arg	His	Asp	Phe	Phe	Lys	Ser	Ala	Met	Pro	Glu	Gly	Tyr	Val	Gln	Glu	
				85						90					95		
5	cgc	acc	atc	ttc	ttc	aag	gac	gac	ggc	aac	tac	aag	acc	cgc	gcc	gag	336
	Arg	Thr	Ile	Phe	Phe	Lys	Asp	Asp	Gly	Asn	Tyr	Lys	Thr	Arg	Ala	Glu	
				100					105					110			
10	gtg	aag	ttc	gag	ggc	gac	acc	ctg	gtg	aac	cgc	atc	gag	ctg	aag	ggc	384
	Val	Lys	Phe	Glu	Gly	Asp	Thr	Leu	Val	Asn	Arg	Ile	Glu	Leu	Lys	Gly	
				115				120					125				
15	atc	gac	ttc	aag	gag	gac	ggc	aac	atc	ctg	ggg	cac	aag	ctg	gag	tac	432
	Ile	Asp	Phe	Lys	Glu	Asp	Gly	Asn	Ile	Leu	Gly	His	Lys	Leu	Glu	Tyr	
		130					135					140					
20	aac	tac	aac	agc	cac	aac	gtc	tat	atc	atg	gcc	gac	aag	cag	aag	aac	480
	Asn	Tyr	Asn	Ser	His	Asn	Val	Tyr	Ile	Met	Ala	Asp	Lys	Gln	Lys	Asn	
		145				150					155					160	
	ggc	atc	aag	gtg	aac	ttc	aag	atc	cgc	cac	aac	atc	gag	gac			522
	Gly	Ile	Lys	Val	Asn	Phe	Lys	Ile	Arg	His	Asn	Ile	Glu	Asp			
					165				170								
25	CFP F1E, F64L mutation, pos. 1 Met removed																
	SEQ ID NOS:764 & 765																
30	gtg	agc	aag	ggc	gag	gag	ctg	ttc	acc	ggg	gtg	gtg	ccc	atc	ctg	gtc	48
	Val	Ser	Lys	Gly	Glu	Glu	Leu	Phe	Thr	Gly	Val	Val	Pro	Ile	Leu	Val	
	1				5					10					15		
	gag	ctg	gac	ggc	gac	gta	aac	ggc	cac	aag	ttc	agc	gtg	tcc	ggc	gag	96
	Glu	Leu	Asp	Gly	Asp	Val	Asn	Gly	His	Lys	Phe	Ser	Val	Ser	Gly	Glu	
				20				25						30			
35	ggc	gag	ggc	gat	gcc	acc	tac	ggc	aag	ctg	acc	ctg	aag	ttc	atc	tgc	144
	Gly	Glu	Gly	Asp	Ala	Thr	Tyr	Gly	Lys	Leu	Thr	Leu	Lys	Phe	Ile	Cys	
			35					40					45				
40	acc	acc	ggc	aag	ctg	ccc	gtg	ccc	tgg	ccc	acc	ctc	gtg	acc	acc	ctg	192
	Thr	Thr	Gly	Lys	Leu	Pro	Val	Pro	Trp	Pro	Thr	Leu	Val	Thr	Thr	Leu	
			50				55					60					
45	ggc	tac	ggc	ctg	cag	tgc	ttc	gcc	cgc	tac	ccc	gac	cac	atg	aag	cgg	240
	Gly	Tyr	Gly	Leu	Gln	Cys	Phe	Ala	Arg	Tyr	Pro	Asp	His	Met	Lys	Arg	
	65					70					75					80	
50	cac	gac	ttc	ttc	aag	tcc	gcc	atg	ccc	gaa	ggc	tac	gtc	cag	gag	cgc	288
	His	Asp	Phe	Phe													

	gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac	432
	Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn	
	130 135 140	
5	tac aac agc cac aac gtc tat atc atg gcc gac aag cag aag aac ggc	480
	Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly	
	145 150 155 160	
10	atc aag gtg aac ttc aag atc cgc cac aac atc gag gac	519
	Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp	
	165 170	
15	CFP F1E, F64L,S65T,Y66W mutations	
	SEQ ID NOS:766 & 767	
	atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg	48
	Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu	
20	1 5 10 15	
	gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc	96
	Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly	
	20 25 30	
25	gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc	144
	Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile	
	35 40 45	
30	tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc	192
	Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr	
	50 55 60	
	ctg acc tgg ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag	240
35	Leu Thr Trp Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys	
	65 70 75 80	
	cgg cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag	288
	Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu	
40	85 90 95	
	cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag	336
	Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu	
	100 105 110	
45	gtg aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc	384
	Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly	
	115 120 125	
50	atc gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac	432
	Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr	
	130 135 140	
	aac tac aac agc cac aac gtc tat atc atg gcc gac aag cag aag aac	480
55	Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn	
	145 150 155 160	

ggc atc aag gtg aac ttc aag atc cgc cac aac atc gag gac 522  
 Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp  
                   165                  170

5

CFP F1E, F64L,S65T,Y66W mutations, pos. 1 Met removed  
 SEQ ID NOS:768 & 769

10 gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc 48  
 Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val  
   1                  5                  10                  15

15 gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag 96  
 Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu  
                   20                  25                  30

20 ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc tgc 144  
 Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys  
                   35                  40                  45

25 acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ctg 192  
 Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Leu  
                   50                  55                  60

acc tgg ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag cgg 240  
 Thr Trp Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg  
   65                  70                  75                  80

30 cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc 288  
 His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg  
                   85                  90                  95

35 acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag gtg 336  
 Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val  
                   100                  105                  110

40 aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc atc 384  
 Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile  
                   115                  120                  125

45 gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac 432  
 Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn  
                   130                  135                  140

50 tac aac agc cac aac gtc tat atc atg gcc gac aag cag aag aac ggc 480  
 Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly  
   145                  150                  155                  160

50 atc aag gtg aac ttc aag atc cgc cac aac atc gag gac 519  
 Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp  
                   165                  170

55

CFP F1E, F64L,S65T,Y66W,N146I,M153T, V163A mutations  
SEQ ID NOS:770 & 771

5	atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu 1 5 10 15	48
10	gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly 20 25 30	96
15	gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile 35 40 45	144
20	tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr 50 55 60	192
25	ctg acc tgg ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag Leu Thr Trp Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys 65 70 75 80	240
30	cgg cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu 85 90 95	288
35	cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu 100 105 110	336
40	gtg aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly 115 120 125	384
45	atc gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr 130 135 140	432
50	aac tac atc agc cac aac gtc tat atc acc gcc gac aag cag aag aac Asn Tyr Ile Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn 145 150 155 160	480
55	ggc atc aag gcc aac ttc aag atc cgc cac aac atc gag gac Gly Ile Lys Ala Asn Phe Lys Ile Arg His Asn Ile Glu Asp 165 170	522

CFP F1E, F64L,S65T,Y66W,N146I,M153T,V163A mutations, pos. 1 Met removed  
SEQ ID NOS:772 & 773

55	gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val 1 5 10 15	48
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	gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag	96
	Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu	
	20 25 30	
5	ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc tgc	144
	Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys	
	35 40 45	
10	acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ctg	192
	Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Leu	
	50 55 60	
15	acc tgg ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag cgg	240
	Thr Trp Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg	
	65 70 75 80	
20	cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc	288
	His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg	
	85 90 95	
25	acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag gtg	336
	Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val	
	100 105 110	
30	aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc atc	384
	Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile	
	115 120 125	
35	gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac	432
	Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn	
	130 135 140	
40	tac atc agc cac aac gtc tat atc acc gcc gac aag cag aag aac ggc	480
	Tyr Ile Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly	
	145 150 155 160	
45	atc aag gcc aac ttc aag atc cgc cac aac atc gag gac	519
	Ile Lys Ala Asn Phe Lys Ile Arg His Asn Ile Glu Asp	
	165 170	
50	CFP F1E, Y66W mutation	
	SEQ ID NOS:774 & 775	
55	atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg	48
	Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu	
	1 5 10 15	
60	gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc	96
	Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly	
	20 25 30	
65	gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc	144
	Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile	
	35 40 45	



	tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc	192
	Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr	
	50 55 60	
5	ttc ggc tgg ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag	240
	Phe Gly Trp Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys	
	65 70 75 80	
10	cgg cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag	288
	Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu	
	85 90 95	
15	cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag	336
	Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu	
	100 105 110	
20	gtg aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc	384
	Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly	
	115 120 125	
25	atc gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac	432
	Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr	
	130 135 140	
30	aac tac aac agc cac aac gtc tat atc atg gcc gac aag cag aag aac	480
	Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn	
	145 150 155 160	
35	ggc atc aag gtg aac ttc aag atc cgc cac aac atc gag gac	522
	Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp	
	165 170	
40	CFP F1E,Y66W mutation, pos. 1 Met removed	
	SEQ ID NOS:776 & 777	
45	gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc	48
	Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val	
	1 5 10 15	
50	gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag	96
	Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu	
	20 25 30	
55	ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc tgc	144
	Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys	
	35 40 45	
60	acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ttc	192
	Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe	
	50 55 60	
65	ggc tgg ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag cgg	240
	Gly Trp Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg	
	65 70 75 80	

	cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc	288
	His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg	
	85 90 95	
5	acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag gtg	336
	Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val	
	100 105 110	
10	aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc atc	384
	Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile	
	115 120 125	
15	gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac	432
	Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn	
	130 135 140	
20	tac aac agc cac aac gtc tat atc atg gcc gac aag cag aag aac ggc	480
	Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly	
	145 150 155 160	
25	atc aag gtg aac ttc aag atc cgc cac aac atc gag gac	519
	Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp	
	165 170	
	CFP F1E, Y66W, N146I mutations	
	SEQ ID NOS:778 & 779	
30	atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg	48
	Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu	
	1 5 10 15	
35	gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc	96
	Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly	
	20 25 30	
40	gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc	144
	Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile	
	35 40 45	
45	tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc	192
	Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr	
	50 55 60	
50	ttc ggc tgg ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag	240
	Phe Gly Trp Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys	
	65 70 75 80	
55	cgg cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag	288
	Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu	
	85 90 95	
55	cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag	336
	Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu	
	100 105 110	

	gtg aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc	384
	Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly	
	115 120 125	
5	atc gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac	432
	Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr	
	130 135 140	
10	aac tac atc agc cac aac gtc tat atc atg gcc gac aag cag aag aac	480
	Asn Tyr Ile Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn	
	145 150 155 160	
15	ggc atc aag gtg aac ttc aag atc cgc cac aac atc gag gac	522
	Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp	
	165 170	
20	CFP F1E, Y66W, N146I mutations, pos. 1 Met removed	
	SEQ ID NOS:780 & 781	
25	gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc	48
	Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val	
	1 5 10 15	
30	gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag	96
	Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu	
	20 25 30	
35	ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc tgc	144
	Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys	
	35 40 45	
40	acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ttc	192
	Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe	
	50 55 60	
45	ggc tgg ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag cgg	240
	Gly Trp Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg	
	65 70 75 80	
50	cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc	288
	His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg	
	85 90 95	
55	acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag gtg	336
	Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val	
	100 105 110	
60	aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc atc	384
	Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile	
	115 120 125	
65	gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac	432
	Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn	
	130 135 140	

	tac atc agc cac aac gtc tat atc atg gcc gac aag cag aag aac ggc	480
	Tyr Ile Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly	
	145 150 155 160	
5	atc aag gtg aac ttc aag atc cgc cac aac atc gag gac	519
	Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp	
	165 170	
10	CFP F1E, M153T mutation	
	SEQ ID NOS:782 & 783	
	atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg	48
	Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu	
15	1 5 10 15	
	gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc	96
	Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly	
	20 25 30	
20	gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc	144
	Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile	
	35 40 45	
25	tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc	192
	Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr	
	50 55 60	
	ttc ggc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag	240
30	Phe Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys	
	65 70 75 80	
	cgg cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag	288
	Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu	
35	85 90 95	
	cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag	336
	Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu	
	100 105 110	
40	gtg aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc	384
	Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly	
	115 120 125	
45	atc gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac	432
	Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr	
	130 135 140	
	aac tac aac agc cac aac gtc tat atc acc gcc gac aag cag aag aac	480
50	Asn Tyr Asn Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn	
	145 150 155 160	
	ggc atc aag gtg aac ttc aag atc cgc cac aac atc gag gac	522
	Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp	
55	165 170	

CFP F1E, M153T mutation, pos. 1 Met removed  
SEQ ID NOS:784 & 785

5	gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val 1 5 10 15	48
10	gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu 20 25 30	96
15	ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc tgc Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys 35 40 45	144
20	acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ttc Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe 50 55 60	192
25	ggc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag cgg Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg 65 70 75 80	240
30	cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg 85 90 95	288
35	acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag gtg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val 100 105 110	336
40	aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc atc Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile 115 120 125	384
45	gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn 130 135 140	432
50	tac aac agc cac aac gtc tat atc acc gcc gac aag cag aag aac ggc Tyr Asn Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly 145 150 155 160	480
55	atc aag gtg aac ttc aag atc cgc cac aac atc gag gac Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp 165 170	519

CFP F1E, N146I, M153T mutations  
SEQ ID NOS:786 & 787

50	atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu 1 5 10 15	48
55	gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly 20 25 30	96

	gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc	144
	Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile	
	35 40 45	
5	tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc	192
	Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr	
	50 55 60	
10	ttc ggc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag	240
	Phe Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys	
	65 70 75 80	
15	cgg cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag	288
	Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu	
	85 90 95	
20	cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag	336
	Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu	
	100 105 110	
25	gtg aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc	384
	Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly	
	115 120 125	
30	atc gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac	432
	Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr	
	130 135 140	
35	aac tac atc agc cac aac gtc tat atc acc gcc gac aag cag aag aac	480
	Asn Tyr Ile Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn	
	145 150 155 160	
40	ggc atc aag gtg aac ttc aag atc cgc cac aac atc gag gac	522
	Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp	
	165 170	
40	CFP F1E, N146I, M153T mutations, pos. 1 Met removed	
	SEQ ID NOS:788 & 789	
45	gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc	48
	Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val	
	1 5 10 15	
50	gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag	96
	Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu	
	20 25 30	
55	ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc tgc	144
	Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys	
	35 40 45	
55	acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ttc	192
	Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe	
	50 55 60	

	ggc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag cgg	240
	Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg	
	65 70 75 80	
5	cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc	288
	His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg	
	85 90 95	
10	acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag gtg	336
	Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val	
	100 105 110	
15	aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc atc	384
	Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile	
	115 120 125	
20	gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac	432
	Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn	
	130 135 140	
25	tac atc agc cac aac gtc tat atc acc gcc gac aag cag aag aac ggc	480
	Tyr Ile Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly	
	145 150 155 160	
30	atc aag gtg aac ttc aag atc cgc cac aac atc gag gac	519
	Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp	
	165 170	
30	CFP F1E, N146I, M153T, V163A mutations	
	SEQ ID NOS:790 & 791	
35	atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg	48
	Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu	
	1 5 10 15	
40	gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc	96
	Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly	
	20 25 30	
45	gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc	144
	Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile	
	35 40 45	
50	tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc	192
	Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr	
	50 55 60	
55	ttc ggc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag	240
	Phe Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys	
	65 70 75 80	
55	cgg cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag	288
	Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu	
	85 90 95	

	cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag	336
	Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu	
	100 105 110	
5	gtg aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc	384
	Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly	
	115 120 125	
10	atc gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac	432
	Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr	
	130 135 140	
15	aac tac atc agc cac aac gtc tat atc acc gcc gac aag cag aag aac	480
	Asn Tyr Ile Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn	
	145 150 155 160	
20	ggc atc aag gcc aac ttc aag atc cgc cac aac atc gag gac	522
	Gly Ile Lys Ala Asn Phe Lys Ile Arg His Asn Ile Glu Asp	
	165 170	
	CFP F1E, N146I, M153T, V163A mutations, pos. 1 Met removed	
25	SEQ ID NOS:792 & 793	
	gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc	48
	Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val	
	1 5 10 15	
30	gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag	96
	Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu	
	20 25 30	
35	ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc tgc	144
	Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys	
	35 40 45	
40	acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ttc	192
	Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe	
	50 55 60	
45	ggc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag cgg	240
	Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg	
	65 70 75 80	
	cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc	288
	His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg	
	85 90 95	
50	acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag gtg	336
	Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val	
	100 105 110	
55	aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc atc	384
	Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile	
	115 120 125	



	gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac	432
	Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn	
	130 135 140	
5	tac atc agc cac aac gtc tat atc acc gcc gac aag cag aag aac ggc	480
	Tyr Ile Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly	
	145 150 155 160	
10	atc aag gcc aac ttc aag atc cgc cac aac atc gag gac	519
	Ile Lys Ala Asn Phe Lys Ile Arg His Asn Ile Glu Asp	
	165 170	
15	CFP F1E, Y66W,N146I,M153T mutations	
	SEQ ID NOS:794 & 795	
20	atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg	48
	Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu	
	1 5 10 15	
	gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc	96
	Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly	
	20 25 30	
25	gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc	144
	Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile	
	35 40 45	
30	tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc	192
	Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr	
	50 55 60	
35	ttc ggc tgg ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag	240
	Phe Gly Trp Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys	
	65 70 75 80	
40	cgg cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag	288
	Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu	
	85 90 95	
	cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag	336
	Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu	
	100 105 110	
45	gtg aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc	384
	Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly	
	115 120 125	
50	atc gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac	432
	Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr	
	130 135 140	
55	aac tac atc agc cac aac gtc tat atc acc gcc gac aag cag aag aac	480
	Asn Tyr Ile Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn	
	145 150 155 160	

ggc atc aag gtg aac ttc aag atc cgc cac aac atc gag gac 522  
 Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp  
 165 170

5

CFP F1E, Y66W, N146I, and M153T mutations, pos. 1 Met removed  
 SEQ ID NOS:796 & 797

10 gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc 48  
 Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val  
 1 5 10 15

15 gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag 96  
 Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu  
 20 25 30

20 ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc tgc 144  
 Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys  
 35 40 45

25 acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ttc 192  
 Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe  
 50 55 60

ggc tgg ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag cgg 240  
 Gly Trp Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg  
 65 70 75 80

30 cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc 288  
 His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg  
 85 90 95

35 acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag gtg 336  
 Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val  
 100 105 110

40 aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc atc 384  
 Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile  
 115 120 125

45 gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac 432  
 Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn  
 130 135 140

50 tac atc agc cac aac gtc tat atc acc gcc gac aag cag aag aac ggc 480  
 Tyr Ile Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly  
 145 150 155 160

atc aag gtg aac ttc aag atc cgc cac aac atc gag gac 519  
 Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp  
 165 170

55

CFP F1E, Y66W, N146I, M153T, V163A mutations  
SEQ ID NOS:798 & 799

5	atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu 1 5 10 15	48
10	gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly 20 25 30	96
15	gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile 35 40 45	144
20	tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr 50 55 60	192
25	ttc ggc tgg ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag Phe Gly Trp Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys 65 70 75 80	240
30	cgg cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu 85 90 95	288
35	cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu 100 105 110	336
40	gtg aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly 115 120 125	384
45	atc gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr 130 135 140	432
50	aac tac atc agc cac aac gtc tat atc acc gcc gac aag cag aag aac Asn Tyr Ile Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn 145 150 155 160	480
55	ggc atc aag gcc aac ttc aag atc cgc cac aac atc gag gac Gly Ile Lys Ala Asn Phe Lys Ile Arg His Asn Ile Glu Asp 165 170	522

CFP F1E, Y66W, N146I, M153T, V163A mutations, pos. 1 Met removed  
SEQ ID NOS:800 & 801

55	gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val 1 5 10 15	48
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	gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag	96
	Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu	
	20 25 30	
5	ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc tgc	144
	Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys	
	35 40 45	
10	acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ttc	192
	Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe	
	50 55 60	
15	ggc tgg ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag cgg	240
	Gly Trp Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg	
	65 70 75 80	
20	cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc	288
	His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg	
	85 90 95	
25	acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag gtg	336
	Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val	
	100 105 110	
30	aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc atc	384
	Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile	
	115 120 125	
35	gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac	432
	Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn	
	130 135 140	
40	tac atc agc cac aac gtc tat atc acc gcc gac aag cag aag aac ggc	480
	Tyr Ile Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly	
	145 150 155 160	
45	atc aag gcc aac ttc aag atc cgc cac aac atc gag gac	519
	Ile Lys Ala Asn Phe Lys Ile Arg His Asn Ile Glu Asp	
	165 170	
50	CFP FlE, S65A mutation	
	SEQ ID NOS:802 & 803	
55	atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg	48
	Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu	
	1 5 10 15	
60	gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc	96
	Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly	
	20 25 30	
65	gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc	144
	Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile	
	35 40 45	

	tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc	192
	Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr	
	50 55 60	
5	ttc gcc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag	240
	Phe Ala Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys	
	65 70 75 80	
10	cgg cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag	288
	Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu	
	85 90 95	
15	cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag	336
	Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu	
	100 105 110	
20	gtg aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc	384
	Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly	
	115 120 125	
25	atc gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac	432
	Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr	
	130 135 140	
30	aac tac aac agc cac aac gtc tat atc atg gcc gac aag cag aag aac	480
	Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn	
	145 150 155 160	
35	ggc atc aag gtg aac ttc aag atc cgc cac aac atc gag gac	522
	Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp	
	165 170	
40	CFP FlE, S65A mutation, pos. 1 Met removed	
	SEQ ID NOS:804 & 805	
45	gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc	48
	Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val	
	1 5 10 15	
50	gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag	96
	Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu	
	20 25 30	
55	ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc tgc	144
	Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys	
	35 40 45	
60	acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ttc	192
	Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe	
	50 55 60	
65	gcc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag cgg	240
	Ala Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg	
	65 70 75 80	

	cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc	288
	His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg	
	85 90 95	
5	acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag gtg	336
	Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val	
	100 105 110	
10	aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc atc	384
	Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile	
	115 120 125	
15	gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac	432
	Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn	
	130 135 140	
20	tac aac agc cac aac gtc tat atc atg gcc gac aag cag aag aac ggc	480
	Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly	
	145 150 155 160	
	atc aag gtg aac ttc aag atc cgc cac aac atc gag gac	519
	Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp	
	165 170	
25		
	CFP F1E, S65A, Y66W, S72A mutations	
	SEQ ID NOS:806 & 807	
30	atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg	48
	Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu	
	1 5 10 15	
35	gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc	96
	Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly	
	20 25 30	
40	gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc	144
	Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile	
	35 40 45	
45	tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc	192
	Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr	
	50 55 60	
	ttc gcc tgg ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag	240
	Phe Ala Trp Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys	
	65 70 75 80	
50	cgg cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag	288
	Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu	
	85 90 95	
55	cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag	336
	Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu	
	100 105 110	

	gtg aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc	384
	Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly	
	115 120 125	
5	atc gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac	432
	Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr	
	130 135 140	
10	aac tac aac agc cac aac gtc tat atc atg gcc gac aag cag aag aac	480
	Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn	
	145 150 155 160	
	ggc atc aag gtg aac ttc aag atc cgc cac aac atc gag gac	522
	Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp	
15	165 170	
20	CFP F1E, S65A, Y66W, and S72A mutations, pos. 1 Met removed SEQ ID NOS:808 & 809	
	gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc	48
	Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val	
25	1 5 10 15	
	gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag	96
	Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu	
	20 25 30	
30	ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc tgc	144
	Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys	
	35 40 45	
35	acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ttc	192
	Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe	
	50 55 60	
40	gcc tgg ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag cgg	240
	Ala Trp Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg	
	65 70 75 80	
	cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc	288
	His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg	
45	85 90 95	
	acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag gtg	336
	Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val	
	100 105 110	
50	aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc atc	384
	Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile	
	115 120 125	
55	gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac	432
	Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn	
	130 135 140	

	tac aac agc cac aac gtc tat atc atg gcc gac aag cag aag aac ggc	480
	Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly	
	145 150 155 160	
5	atc aag gtg aac ttc aag atc cgc cac aac atc gag gac	519
	Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp	
	165 170	
10	CFP F1E, S65A, Y66W, S72A, N146I, M153T, and V163A mutations SEQ ID NOS:810 & 811	
15	atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg	48
	Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu	
	1 5 10 15	
20	gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc	96
	Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly	
	20 25 30	
25	gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc	144
	Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile	
	35 40 45	
30	tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc	192
	Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr	
	50 55 60	
35	ttc gcc tgg ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag	240
	Phe Ala Trp Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys	
	65 70 75 80	
40	cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag	288
	Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu	
	85 90 95	
45	cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag	336
	Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu	
	100 105 110	
50	gtg aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc	384
	Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly	
	115 120 125	
55	atc gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac	432
	Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr	
	130 135 140	
60	aac tac atc agc cac aac gtc tat atc acc gcc gac aag cag aag aac	480
	Asn Tyr Ile Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn	
	145 150 155 160	
65	ggc atc aag gcc aac ttc aag atc cgc cac aac atc gag gac	522
	Gly Ile Lys Ala Asn Phe Lys Ile Arg His Asn Ile Glu Asp	
	165 170	



CFP F1E, S65A,Y66W,S72A,N146I,M153T,V163A mutations,pos. 1 Met removed  
SEQ ID NOS:812 & 813

5	gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val 1 5 10 15	48
10	gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu 20 25 30	96
15	ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc tgc Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys 35 40 45	144
20	acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ttc Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe 50 55 60	192
25	gcc tgg ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag cgg Ala Trp Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg 65 70 75 80	240
30	cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg 85 90 95	288
35	acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag gtg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val 100 105 110	336
40	aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc atc Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile 115 120 125	384
45	gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn 130 135 140	432
50	tac atc agc cac aac gtc tat atc acc gcc gac aag cag aag aac ggc Tyr Ile Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly 145 150 155 160	480
55	atc aag gcc aac ttc aag atc cgc cac aac atc gag gac Ile Lys Ala Asn Phe Lys Ile Arg His Asn Ile Glu Asp 165 170	519
BFP F1E, Y66H mutation SEQ ID NOS:814 & 815		
55	atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu 1 5 10 15	48

	gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc	96
	Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly	
	20 25 30	
5	gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc	144
	Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile	
	35 40 45	
10	tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc	192
	Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr	
	50 55 60	
15	ttc ggc cac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag	240
	Phe Gly His Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys	
	65 70 75 80	
20	cgg cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag	288
	Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu	
	85 90 95	
25	cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag	336
	Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu	
	100 105 110	
30	gtg aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc	384
	Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly	
	115 120 125	
35	atc gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac	432
	Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr	
	130 135 140	
40	aac tac aac agc cac aac gtc tat atc atg gcc gac aag cag aag aac	480
	Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn	
	145 150 155 160	
45	ggc atc aag gtg aac ttc aag atc cgc cac aac atc gag gac	522
	Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp	
	165 170	
BFP F1E, Y66H mutation, pos. 1 Met removed		
SEQ ID NOS:816 & 817		
50	gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc	48
	Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val	
	1 5 10 15	
55	gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag	96
	Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu	
	20 25 30	
60	ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc tgc	144
	Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys	
	35 40 45	

	acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ttc	192
	Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe	
	50 55 60	
5	ggc cac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag cgg	240
	Gly His Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg	
	65 70 75 80	
10	cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc	288
	His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg	
	85 90 95	
15	acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag gtg	336
	Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val	
	100 105 110	
20	aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc atc	384
	Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile	
	115 120 125	
25	gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac	432
	Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn	
	130 135 140	
30	tac aac agc cac aac gtc tat atc atg gcc gac aag cag aag aac ggc	480
	Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly	
	145 150 155 160	
35	atc aag gtg aac ttc aag atc cgc cac aac atc gag gac	519
	Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp	
	165 170	
35	BFP F1E, F64L,Y66H mutations	
	SEQ ID NOS:818 & 819	
40	atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg	48
	Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu	
	1 5 10 15	
45	gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc	96
	Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly	
	20 25 30	
50	gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc	144
	Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile	
	35 40 45	
55	tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc	192
	Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr	
	50 55 60	
55	ctc ggc cac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag	240
	Leu Gly His Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys	
	65 70 75 80	

	cgg	cac	gac	ttc	ttc	aag	tcc	gcc	atg	ccc	gaa	ggc	tac	gtc	cag	gag	288
	Arg	His	Asp	Phe	Phe	Lys	Ser	Ala	Met	Pro	Glu	Gly	Tyr	Val	Gln	Glu	
				85						90					95		
5	cgc	acc	atc	ttc	ttc	aag	gac	gac	ggc	aac	tac	aag	acc	cgc	gcc	gag	336
	Arg	Thr	Ile	Phe	Phe	Lys	Asp	Asp	Gly	Asn	Tyr	Lys	Thr	Arg	Ala	Glu	
				100					105					110			
10	gtg	aag	ttc	gag	ggc	gac	acc	ctg	gtg	aac	cgc	atc	gag	ctg	aag	ggc	384
	Val	Lys	Phe	Glu	Gly	Asp	Thr	Leu	Val	Asn	Arg	Ile	Glu	Leu	Lys	Gly	
				115				120					125				
15	atc	gac	ttc	aag	gag	gac	ggc	aac	atc	ctg	ggg	cac	aag	ctg	gag	tac	432
	Ile	Asp	Phe	Lys	Glu	Asp	Gly	Asn	Ile	Leu	Gly	His	Lys	Leu	Glu	Tyr	
		130					135					140					
20	aac	tac	aac	agc	cac	aac	gtc	tat	atc	atg	gcc	gac	aag	cag	aag	aac	480
	Asn	Tyr	Asn	Ser	His	Asn	Val	Tyr	Ile	Met	Ala	Asp	Lys	Gln	Lys	Asn	
		145				150					155					160	
	ggc	atc	aag	gtg	aac	ttc	aag	atc	cgc	cac	aac	atc	gag	gac			522
	Gly	Ile	Lys	Val	Asn	Phe	Lys	Ile	Arg	His	Asn	Ile	Glu	Asp			
					165					170							
25	BFP F1E, F64L,Y66H mutations, pos. 1 Met removed																
	SEQ ID NOS:820 & 821																
30	gtg	agc	aag	ggc	gag	gag	ctg	ttc	acc	ggg	gtg	gtg	ccc	atc	ctg	gtc	48
	Val	Ser	Lys	Gly	Glu	Glu	Leu	Phe	Thr	Gly	Val	Val	Pro	Ile	Leu	Val	
	1				5					10					15		
35	gag	ctg	gac	ggc	gac	gta	aac	ggc	cac	aag	ttc	agc	gtg	tcc	ggc	gag	96
	Glu	Leu	Asp	Gly	Asp	Val	Asn	Gly	His	Lys	Phe	Ser	Val	Ser	Gly	Glu	
				20				25						30			
40	ggc	gag	ggc	gat	gcc	acc	tac	ggc	aag	ctg	acc	ctg	aag	ttc	atc	tgc	144
	Gly	Glu	Gly	Asp	Ala	Thr	Tyr	Gly	Lys	Leu	Thr	Leu	Lys	Phe	Ile	Cys	
			35					40					45				
45	acc	acc	ggc	aag	ctg	ccc	gtg	ccc	tgg	ccc	acc	ctc	gtg	acc	acc	ctc	192
	Thr	Thr	Gly	Lys	Leu	Pro	Val	Pro	Trp	Pro	Thr	Leu	Val	Thr	Thr	Leu	
		50					55					60					
	ggc	cac	ggc	ctg	cag	tgc	ttc	gcc	cgc	tac	ccc	gac	cac	atg	aag	cgg	240
	Gly	His	Gly	Leu	Gln	Cys	Phe	Ala	Arg	Tyr	Pro	Asp	His	Met	Lys	Arg	
		65				70				75					80		
50	cac	gac	ttc	ttc	aag	tcc	gcc	atg	ccc	gaa	ggc	tac	gtc	cag	gag	cgc	288
	His	Asp	Phe	Phe	Lys	Ser	Ala	Met	Pro	Glu	Gly	Tyr	Val	Gln	Glu	Arg	
					85					90					95		
55	acc	atc	ttc	ttc	aag	gac	gac	ggc	aac	tac	aag	acc	cgc	gcc	gag	gtg	336
	Thr	Ile	Phe	Phe	Lys	Asp	Asp	Gly	Asn	Tyr	Lys	Thr	Arg	Ala	Glu	Val	
				100				105						110			

	aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc atc	384
	Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile	
	115 120 125	
5	gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac	432
	Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn	
	130 135 140	
10	tac aac agc cac aac gtc tat atc atg gcc gac aag cag aag aac ggc	480
	Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly	
	145 150 155 160	
	atc aag gtg aac ttc aag atc cgc cac aac atc gag gac	519
15	Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp	
	165 170	
20	BFP F1E, F64L, Y66H, Y145F mutations	
	SEQ ID NOS:822 & 823	
	atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg	48
	Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu	
	1 5 10 15	
25	gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc	96
	Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly	
	20 25 30	
30	gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc	144
	Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile	
	35 40 45	
35	tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc	192
	Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr	
	50 55 60	
40	ctc ggc cac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag	240
	Leu Gly His Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys	
	65 70 75 80	
	cgg cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag	288
	Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu	
	85 90 95	
45	cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag	336
	Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu	
	100 105 110	
50	gtg aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc	384
	Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly	
	115 120 125	
55	atc gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac	432
	Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr	
	130 135 140	

	aac	ttc	aac	agc	cac	aac	gtc	tat	atc	atg	gcc	gac	aag	cag	aag	aac	480
	Asn	Phe	Asn	Ser	His	Asn	Val	Tyr	Ile	Met	Ala	Asp	Lys	Gln	Lys	Asn	
	145					150					155					160	
5	ggc	atc	aag	gtg	aac	ttc	aag	atc	cgc	cac	aac	atc	gag	gac			522
	Gly	Ile	Lys	Val	Asn	Phe	Lys	Ile	Arg	His	Asn	Ile	Glu	Asp			
					165					170							
10	BFP F1E, F64L, Y66H, Y145F mutations, pos. 1 Met removed SEQ ID NOS:824 & 825																
	gtg	agc	aag	ggc	gag	gag	ctg	ttc	acc	ggg	gtg	gtg	ccc	atc	ctg	gtc	48
	Val	Ser	Lys	Gly	Glu	Glu	Leu	Phe	Thr	Gly	Val	Val	Pro	Ile	Leu	Val	
15	1				5					10					15		
	gag	ctg	gac	ggc	gac	gta	aac	ggc	cac	aag	ttc	agc	gtg	tcc	ggc	gag	96
	Glu	Leu	Asp	Gly	Asp	Val	Asn	Gly	His	Lys	Phe	Ser	Val	Ser	Gly	Glu	
				20					25					30			
20	ggc	gag	ggc	gat	gcc	acc	tac	ggc	aag	ctg	acc	ctg	aag	ttc	atc	tgc	144
	Gly	Glu	Gly	Asp	Ala	Thr	Tyr	Gly	Lys	Leu	Thr	Leu	Lys	Phe	Ile	Cys	
			35					40					45				
25	acc	acc	ggc	aag	ctg	ccc	gtg	ccc	tgg	ccc	acc	ctc	gtg	acc	acc	ctc	192
	Thr	Thr	Gly	Lys	Leu	Pro	Val	Pro	Trp	Pro	Thr	Leu	Val	Thr	Thr	Leu	
		50					55					60					
	ggc	cac	ggc	ctg	cag	tgc	ttc	gcc	cgc	tac	ccc	gac	cac	atg	aag	cgg	240
30	Gly	His	Gly	Leu	Gln	Cys	Phe	Ala	Arg	Tyr	Pro	Asp	His	Met	Lys	Arg	
	65					70					75					80	
	cac	gac	ttc	ttc	aag	tcc	gcc	atg	ccc	gaa	ggc	tac	gtc	cag	gag	cgc	288
	His	Asp	Phe	Phe	Lys	Ser	Ala	Met	Pro	Glu	Gly	Tyr	Val	Gln	Glu	Arg	
35					85					90					95		
	acc	atc	ttc	ttc	aag	gac	gac	ggc	aac	tac	aag	acc	cgc	gcc	gag	gtg	336
	Thr	Ile	Phe	Phe	Lys	Asp	Asp	Gly	Asn	Tyr	Lys	Thr	Arg	Ala	Glu	Val	
				100					105					110			
40	aag	ttc	gag	ggc	gac	acc	ctg	gtg	aac	cgc	atc	gag	ctg	aag	ggc	atc	384
	Lys	Phe	Glu	Gly	Asp	Thr	Leu	Val	Asn	Arg	Ile	Glu	Leu	Lys	Gly	Ile	
			115					120					125				
45	gac	ttc	aag	gag	gac	ggc	aac	atc	ctg	ggg	cac	aag	ctg	gag	tac	aac	432
	Asp	Phe	Lys	Glu	Asp	Gly	Asn	Ile	Leu	Gly	His	Lys	Leu	Glu	Tyr	Asn	
		130					135					140					
	ttc	aac	agc	cac	aac	gtc	tat	atc	atg	gcc	gac	aag	cag	aag	aac	ggc	480
50	Phe	Asn	Ser	His	Asn	Val	Tyr	Ile	Met	Ala	Asp	Lys	Gln	Lys	Asn	Gly	
	145					150					1						

BFP F1E, Y145F mutation  
SEQ ID NOS:826 & 827

5	atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu 1 5 10 15	48
10	gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly 20 25 30	96
15	gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile 35 40 45	144
20	tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr 50 55 60	192
25	ttc ggc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag Phe Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys 65 70 75 80	240
30	cgg cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu 85 90 95	288
35	cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu 100 105 110	336
40	gtg aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly 115 120 125	384
45	atc gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr 130 135 140	432
50	aac ttc aac agc cac aac gtc tat atc atg gcc gac aag cag aag aac Asn Phe Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn 145 150 155 160	480
55	ggc atc aag gtg aac ttc aag atc cgc cac aac atc gag gac Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp 165 170	522

BFP F1E, Y145F mutation, pos. 1 Met removed  
SEQ ID NOS:828 & 829

55	gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val 1 5 10 15	48
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	gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag	96
	Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu	
	20 25 30	
5	ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc tgc	144
	Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys	
	35 40 45	
10	acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ttc	192
	Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe	
	50 55 60	
15	ggc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag cgg	240
	Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg	
	65 70 75 80	
20	cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc	288
	His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg	
	85 90 95	
25	acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag gtg	336
	Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val	
	100 105 110	
30	aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc atc	384
	Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile	
	115 120 125	
35	gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac	432
	Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn	
	130 135 140	
40	ttc aac agc cac aac gtc tat atc atg gcc gac aag cag aag aac ggc	480
	Phe Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly	
	145 150 155 160	
45	atc aag gtg aac ttc aag atc cgc cac aac atc gag gac	519
	Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp	
	165 170	
Venus F1E, F46L mutation		
SEQ ID NOS:830 & 831		
50	atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg	48
	Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu	
	1 5 10 15	
55	gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc	96
	Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly	
	20 25 30	
60	gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ctg atc	144
	Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Leu Ile	
	35 40 45	



	tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc	192
	Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr	
	50 55 60	
5	ttc ggc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag	240
	Phe Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys	
	65 70 75 80	
10	cgg cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag	288
	Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu	
	85 90 95	
15	cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag	336
	Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu	
	100 105 110	
20	gtg aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc	384
	Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly	
	115 120 125	
25	atc gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac	432
	Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr	
	130 135 140	
30	aac tac aac agc cac aac gtc tat atc atg gcc gac aag cag aag aac	480
	Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn	
	145 150 155 160	
35	ggc atc aag gtg aac ttc aag atc cgc cac aac atc gag gac	522
	Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp	
	165 170	
40	Venus F1E, F46L mutation, pos. 1 Met removed	
	SEQ ID NOS:832 & 833	
45	gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc	48
	Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val	
	1 5 10 15	
50	gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag	96
	Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu	
	20 25 30	
55	ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ctg atc tgc	144
	Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Leu Ile Cys	
	35 40 45	
60	acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ttc	192
	Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe	
	50 55 60	
65	ggc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag cgg	240
	Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg	
	65 70 75 80	

	cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc	288	
	His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg		
	85 90 95		
5	acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag gtg	336	
	Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val		
	100 105 110		
10	aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc atc	384	
	Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile		
	115 120 125		
15	gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac	432	
	Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn		
	130 135 140		
20	tac aac agc cac aac gtc tat atc atg gcc gac aag cag aag aac ggc	480	
	Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly		
	145 150 155 160		
	atc aag gtg aac ttc aag atc cgc cac aac atc gag gac	519	
	Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp		
	165 170		
25	Venus F1E, F46L,F64L mutations		
	SEQ ID NOS:834 & 835		
30	atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg	48	
	Met Val Ser Lys Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu		
	1 5 10 15		
35	gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc	96	
	Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly		
	20 25 30		
40	gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ctg atc	144	
	Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Leu Ile		
	35 40 45		
45	tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc	192	
	Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr		
	50 55 60		
	ctg ggc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag	240	
	Leu Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys		
	65 70 75 80		
50	cgg cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag	288	
	Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu		
	85 90 95		
55	cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag	336	
	Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu		
	100 105 110		

	gtg aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc	384
	Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly	
	115 120 125	
5	atc gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac	432
	Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr	
	130 135 140	
10	aac tac aac agc cac aac gtc tat atc atg gcc gac aag cag aag aac	480
	Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn	
	145 150 155 160	
15	ggc atc aag gtg aac ttc aag atc cgc cac aac atc gag gac	522
	Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp	
	165 170	
20	Venus F1E, F46L,F64L mutations, pos. 1 Met removed	
	SEQ ID NOS:836 & 837	
25	gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc	48
	Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val	
	1 5 10 15	
30	gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag	96
	Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu	
	20 25 30	
35	ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ctg atc tgc	144
	Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Leu Ile Cys	
	35 40 45	
40	acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ctg	192
	Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Leu	
	50 55 60	
45	ggc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag cgg	240
	Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg	
	65 70 75 80	
50	cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc	288
	His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg	
	85 90 95	
55	acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag gtg	336
	Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val	
	100 105 110	
60	aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc atc	384
	Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile	
	115 120 125	
65	gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac	432
	Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn	
	130 135 140	

	tac aac agc cac aac gtc tat atc atg gcc gac aag cag aag aac ggc	480
	Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly	
	145 150 155 160	
5	atc aag gtg aac ttc aag atc cgc cac aac atc gag gac	519
	Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp	
	165 170	
10	Venus FlE, F46L,M153T mutations	
	SEQ ID NOS:838 & 839	
15	atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg	48
	Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu	
	1 5 10 15	
20	gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc	96
	Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly	
	20 25 30	
25	gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ctg atc	144
	Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Leu Ile	
	35 40 45	
30	tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc	192
	Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr	
	50 55 60	
35	ttc ggc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag	240
	Phe Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys	
	65 70 75 80	
40	cgg cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag	288
	Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu	
	85 90 95	
45	cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag	336
	Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu	
	100 105 110	
50	gtg aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc	384
	Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly	
	115 120 125	
55	atc gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac	432
	Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr	
	130 135 140	
60	aac tac aac agc cac aac gtc tat atc acc gcc gac aag cag aag aac	480
	Asn Tyr Asn Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn	
	145 150 155 160	
65	ggc atc aag gtg aac ttc aag atc cgc cac aac atc gag gac	522
	Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp	
	165 170	

Venus F1E, F46L, M153T mutations, pos. 1 Met removed  
SEQ ID NOS:840 & 841

5	gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val 1 5 10 15	48
10	gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu 20 25 30	96
15	ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ctg atc tgc Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Leu Ile Cys 35 40 45	144
20	acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ttc Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe 50 55 60	192
25	ggc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag cgg Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg 65 70 75 80	240
30	cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg 85 90 95	288
35	acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag gtg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val 100 105 110	336
40	aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc atc Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile 115 120 125	384
45	gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn 130 135 140	432
50	tac aac agc cac aac gtc tat atc acc gcc gac aag cag aag aac ggc Tyr Asn Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly 145 150 155 160	480
55	atc aag gtg aac ttc aag atc cgc cac aac atc gag gac Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp 165 170	519

Venus F1E, F64L, M153T mutations  
SEQ ID NOS:842 & 843

55	atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu 1 5 10 15	48
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	gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc	96
	Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly	
	20 25 30	
5	gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc	144
	Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile	
	35 40 45	
10	tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc	192
	Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr	
	50 55 60	
15	ctg ggc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag	240
	Leu Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys	
	65 70 75 80	
20	cgg cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag	288
	Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu	
	85 90 95	
25	cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag	336
	Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu	
	100 105 110	
30	gtg aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc	384
	Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly	
	115 120 125	
35	atc gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac	432
	Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr	
	130 135 140	
40	aac tac aac agc cac aac gtc tat atc atg gcc gac aag cag aag aac	480
	Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn	
	145 150 155 160	
45	ggc atc aag gtg aac ttc aag atc cgc cac aac atc gag gac	522
	Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp	
	165 170	
Venus F1E, F64L,M153T mutations, pos. 1 Met removed		
SEQ ID NOS:844 & 845		
50	gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc	48
	Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val	
	1 5 10 15	
55	gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag	96
	Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu	
	20 25 30	
60	ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc tgc	144
	Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys	
	35 40 45	

	acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ctg	192
	Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Leu	
	50 55 60	
5	ggc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag cgg	240
	Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg	
	65 70 75 80	
10	cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc	288
	His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg	
	85 90 95	
15	acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag gtg	336
	Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val	
	100 105 110	
20	aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc atc	384
	Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile	
	115 120 125	
25	gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac	432
	Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn	
	130 135 140	
30	tac aac agc cac aac gtc tat atc atg gcc gac aag cag aag aac ggc	480
	Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly	
	145 150 155 160	
35	atc aag gtg aac ttc aag atc cgc cac aac atc gag gac	519
	Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp	
	165 170	
35	Venus F1E, F64L, M153T, V163A mutations SEQ ID NOS:846 & 847	
40	atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg	48
	Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu	
	1 5 10 15	
45	gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc	96
	Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly	
	20 25 30	
50	gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc	144
	Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile	
	35 40 45	
55	tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc	192
	Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr	
	50 55 60	
55	ctg ggc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag	240
	Leu Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys	
	65 70 75 80	

	cgg	cac	gac	ttc	ttc	aag	tcc	gcc	atg	ccc	gaa	ggc	tac	gtc	cag	gag	288
	Arg	His	Asp	Phe	Phe	Lys	Ser	Ala	Met	Pro	Glu	Gly	Tyr	Val	Gln	Glu	
				85						90					95		
5	cgc	acc	atc	ttc	ttc	aag	gac	gac	ggc	aac	tac	aag	acc	cgc	gcc	gag	336
	Arg	Thr	Ile	Phe	Phe	Lys	Asp	Asp	Gly	Asn	Tyr	Lys	Thr	Arg	Ala	Glu	
				100					105					110			
10	gtg	aag	ttc	gag	ggc	gac	acc	ctg	gtg	aac	cgc	atc	gag	ctg	aag	ggc	384
	Val	Lys	Phe	Glu	Gly	Asp	Thr	Leu	Val	Asn	Arg	Ile	Glu	Leu	Lys	Gly	
				115				120					125				
15	atc	gac	ttc	aag	gag	gac	ggc	aac	atc	ctg	ggg	cac	aag	ctg	gag	tac	432
	Ile	Asp	Phe	Lys	Glu	Asp	Gly	Asn	Ile	Leu	Gly	His	Lys	Leu	Glu	Tyr	
		130					135					140					
20	aac	tac	aac	agc	cac	aac	gtc	tat	atc	acc	gcc	gac	aag	cag	aag	aac	480
	Asn	Tyr	Asn	Ser	His	Asn	Val	Tyr	Ile	Thr	Ala	Asp	Lys	Gln	Lys	Asn	
		145				150					155					160	
25	ggc	atc	aag	gcc	aac	ttc	aag	atc	cgc	cac	aac	atc	gag	gac			522
	Gly	Ile	Lys	Ala	Asn	Phe	Lys	Ile	Arg	His	Asn	Ile	Glu	Asp			
					165				170								
30	Venus F1E, F64L, M153T, V163A mutations, pos. 1 Met removed SEQ ID NOS:848 & 849																
	gtg	agc	aag	ggc	gag	gag	ctg	ttc	acc	ggg	gtg	gtg	ccc	atc	ctg	gtc	48
	Val	Ser	Lys	Gly	Glu	Glu	Leu	Phe	Thr	Gly	Val	Val	Pro	Ile	Leu	Val	
	1				5					10					15		
35	gag	ctg	gac	ggc	gac	gta	aac	ggc	cac	aag	ttc	agc	gtg	tcc	ggc	gag	96
	Glu	Leu	Asp	Gly	Asp	Val	Asn	Gly	His	Lys	Phe	Ser	Val	Ser	Gly	Glu	
				20				25						30			
40	ggc	gag	ggc	gat	gcc	acc	tac	ggc	aag	ctg	acc	ctg	aag	ttc	atc	tgc	144
	Gly	Glu	Gly	Asp	Ala	Thr	Tyr	Gly	Lys	Leu	Thr	Leu	Lys	Phe	Ile	Cys	
			35					40					45				
45	acc	acc	ggc	aag	ctg	ccc	gtg	ccc	tgg	ccc	acc	ctc	gtg	acc	acc	ctg	192
	Thr	Thr	Gly	Lys	Leu	Pro	Val	Pro	Trp	Pro	Thr	Leu	Val	Thr	Thr	Leu	
		50					55					60					
50	ggc	tac	ggc	ctg	cag	tgc	ttc	gcc	cgc	tac	ccc	gac	cac	atg	aag	cgg	240
	Gly	Tyr	Gly	Leu	Gln	Cys	Phe	Ala	Arg	Tyr	Pro	Asp	His	Met	Lys	Arg	
	65					70				75						80	
55	cac	gac	ttc	ttc	aag	tcc	gcc	atg	ccc	gaa	ggc	tac	gtc	cag	gag	cgc	288
	His	Asp	Phe	Phe	Lys	Ser	Ala	Met	Pro	Glu	Gly	Tyr	Val	Gln	Glu	Arg	
					85					90		</					



	aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc atc	384
	Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile	
	115 120 125	
5		
	gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac	432
	Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn	
	130 135 140	
10		
	tac aac agc cac aac gtc tat atc acc gcc gag aag cag aag aac ggc	480
	Tyr Asn Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly	
	145 150 155 160	
15		
	atc aag gcc aac ttc aag atc cgc cac aac atc gag gac	519
	Ile Lys Ala Asn Phe Lys Ile Arg His Asn Ile Glu Asp	
	165 170	
20	Venus F1E, F46L,M153T,V163A mutations	
	SEQ ID NOS:850 & 851	
25		
	atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg	48
	Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu	
	1 5 10 15	
30		
	gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc	96
	Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly	
	20 25 30	
35		
	gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ctg atc	144
	Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Leu Ile	
	35 40 45	
40		
	tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc	192
	Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr	
	50 55 60	
45		
	ttc ggc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag	240
	Phe Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys	
	65 70 75 80	
50		
	cgg cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag	288
	Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu	
	85 90 95	
55		
	cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag	336
	Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu	
	100 105 110	
60		
	gtg aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc	384
	Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly	
	115 120 125	
65		
	atc gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac	432
	Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr	
	130 135 140	

	aac tac aac agc cac aac gtc tat atc acc gcc gac aag cag aag aac	480
	Asn Tyr Asn Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn	
	145 150 155 160	
5	ggc atc aag gcc aac ttc aag atc cgc cac aac atc gag gac	522
	Gly Ile Lys Ala Asn Phe Lys Ile Arg His Asn Ile Glu Asp	
	165 170	
10	Venus F1E, F46L, M153T, V163A mutations, pos. 1 Met removed SEQ ID NOS:852 & 853	
	gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc	48
	Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val	
15	1 5 10 15	
	gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag	96
	Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu	
	20 25 30	
20	ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ctg atc tgc	144
	Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Leu Ile Cys	
	35 40 45	
25	acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ttc	192
	Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe	
	50 55 60	
	ggc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag cgg	240
30	Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg	
	65 70 75 80	
	cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc	288
	His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg	
35	85 90 95	
	acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag gtg	336
	Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val	
	100 105 110	
40	aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc atc	384
	Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile	
	115 120 125	
45	gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac	432
	Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn	
	130 135 140	
	tac aac agc cac aac gtc tat atc acc gcc gac aag cag aag aac ggc	480
50	Tyr Asn Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly	
	145 150 155 160	
	atc aag gcc aac ttc aag atc cgc cac aac atc gag gac	519
	Ile Lys Ala Asn Phe Lys Ile Arg His Asn Ile Glu Asp	
55	165 170	

Venus F1E, F46L,F64L,M153T,V163A mutations  
SEQ ID NOS:854 & 855

5	atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu 1 5 10 15	48
10	gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly 20 25 30	96
15	gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ctg atc Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Leu Ile 35 40 45	144
20	tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr 50 55 60	192
25	ctg ggc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag Leu Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys 65 70 75 80	240
30	cgg cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu 85 90 95	288
35	cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu 100 105 110	336
40	gtg aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly 115 120 125	384
45	atc gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr 130 135 140	432
50	aac tac aac agc cac aac gtc tat atc acc gcc gac aag cag aag aac Asn Tyr Asn Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn 145 150 155 160	480
55	ggc atc aag gcc aac ttc aag atc cgc cac aac atc gag gac Gly Ile Lys Ala Asn Phe Lys Ile Arg His Asn Ile Glu Asp 165 170	522
Venus F1E, F46L,F64L,M153T,V163A mutations, pos. 1 Met removed SEQ ID NOS:856 & 857		
55	gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val 1 5 10 15	48

	gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag	96
	Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu	
	20 25 30	
5	ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ctg atc tgc	144
	Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Leu Ile Cys	
	35 40 45	
10	acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ctg	192
	Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Leu	
	50 55 60	
15	ggc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag cgg	240
	Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg	
	65 70 75 80	
20	cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc	288
	His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg	
	85 90 95	
	acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag gtg	336
	Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val	
	100 105 110	
25	aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc atc	384
	Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile	
	115 120 125	
30	gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac	432
	Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn	
	130 135 140	
35	tac aac agc cac aac gtc tat atc acc gcc gac aag cag aag aac ggc	480
	Tyr Asn Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly	
	145 150 155 160	
40	atc aag gcc aac ttc aag atc cgc cac aac atc gag gac	519
	Ile Lys Ala Asn Phe Lys Ile Arg His Asn Ile Glu Asp	
	165 170	
	Venus FlE, V163A mutation	
	SEQ ID NOS:858 & 859	
45	atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg	48
	Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu	
	1 5 10 15	
50	gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc	96
	Val Glu Leu Asp Gly Asp Val Asn Gly His_Lys Phe Ser Val Ser Gly	
	20 25 30	
55	gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc	144
	Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile	
	35 40 45	

	tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc	192
	Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr	
	50 55 60	
5	ttc ggc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag	240
	Phe Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys	
	65 70 75 80	
10	cgg cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag	288
	Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu	
	85 90 95	
15	cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag	336
	Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu	
	100 105 110	
20	gtg aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc	384
	Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly	
	115 120 125	
25	atc gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac	432
	Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr	
	130 135 140	
30	aac tac aac agc cac aac gtc tat atc atg gcc gac aag cag aag aac	480
	Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn	
	145 150 155 160	
35	ggc atc aag gcc aac ttc aag atc cgc cac aac atc gag gac	522
	Gly Ile Lys Ala Asn Phe Lys Ile Arg His Asn Ile Glu Asp	
	165 170	
35	Venus F1E, V163A mutation, pos. 1 Met removed	
	SEQ ID NOS:860 & 861	
40	gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc	48
	Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val	
	1 5 10 15	
45	gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag	96
	Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu	
	20 25 30	
50	ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc tgc	144
	Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys	
	35 40 45	
55	acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ttc	192
	Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe	
	50 55 60	
55	ggc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag cgg	240
	Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg	
	65 70 75 80	

	cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc	288
	His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg	
	85 90 95	
5	acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag gtg	336
	Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val	
	100 105 110	
10	aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc atc	384
	Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile	
	115 120 125	
15	gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac	432
	Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn	
	130 135 140	
20	tac aac agc cac aac gtc tat atc atg gcc gac aag cag aag aac ggc	480
	Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly	
	145 150 155 160	
25	atc aag gcc aac ttc aag atc cgc cac aac atc gag gac	519
	Ile Lys Ala Asn Phe Lys Ile Arg His Asn Ile Glu Asp	
	165 170	
	Venus F1E, M153T,V163A mutations	
	SEQ ID NOS:862 & 863	
30	atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg	48
	Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu	
	1 5 10 15	
35	gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc	96
	Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly	
	20 25 30	
40	gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc	144
	Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile	
	35 40 45	
45	tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc	192
	Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr	
	50 55 60	
50	ttc ggc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag	240
	Phe Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys	
	65 70 75 80	
55	cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag	336
	Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu	
	100 105 110	

	gtg aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc	384
	Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly	
	115 120 125	
5	atc gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac	432
	Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr	
	130 135 140	
10	aac tac aac agc cac aac gtc tat atc acc gcc gac aag cag aag aac	480
	Asn Tyr Asn Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn	
	145 150 155 160	
15	ggc atc aag gcc aac ttc aag atc cgc cac aac atc gag gac	522
	Gly Ile Lys Ala Asn Phe Lys Ile Arg His Asn Ile Glu Asp	
	165 170	
20	Venus F1E, M153T,V163A mutations, pos. 1 Met removed	
	SEQ ID NOS:864 & 865	
25	gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc	48
	Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val	
	1 5 10 15	
30	gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag	96
	Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu	
	20 25 30	
35	ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc tgc	144
	Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys	
	35 40 45	
40	acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ttc	192
	Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe	
	50 55 60	
45	ggc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag cgg	240
	Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg	
	65 70 75 80	
50	cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc	288
	His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg	
	85 90 95	
55	acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag gtg	336
	Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val	
	100 105 110	
60	aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc atc	384
	Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile	
	115 120 125	
65	gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac	432
	Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn	
	130 135 140	

	tac aac agc cac aac gtc tat atc acc gcc gac aag cag aag aac ggc	480
	Tyr Asn Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly	
	145 150 155 160	
5	atc aag gcc aac ttc aag atc cgc cac aac atc gag gac	519
	Ile Lys Ala Asn Phe Lys Ile Arg His Asn Ile Glu Asp	
	165 170	
10	YFP F2E, Met added @ position 1 (YFP F2E corresponds to aa residues 175-end of YFP) SEQ ID NOS:866 & 867	
15	atg ggc agc gtg cag ctc gcc gac cac tac cag cag aac acc ccc atc	48
	Met Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile	
	1 5 10 15	
20	ggc gac ggc ccc gtg ctg ctg ccc gac aac cac tac ctg agc tac cag	96
	Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Tyr Gln	
	20 25 30	
25	tcc gcc ctg agc aaa gac ccc aac gag aag cgc gat cac atg gtc ctg	144
	Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu	
	35 40 45	
30	ctg gag ttc gtg acc gcc gcc ggg atc act ctc ggc atg gac gag ctg	192
	Leu Glu Phe Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu	
	50 55 60	
35	YFP F2E, Y203F mutation SEQ ID NOS:868 & 869	
40	ggc agc gtg cag ctc gcc gac cac tac cag cag aac acc ccc atc ggc	48
	Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly	
	1 5 10 15	
45	gac ggc ccc gtg ctg ctg ccc gac aac cac tac ctg agc ttc cag tcc	96
	Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Phe Gln Ser	
	20 25 30	
50	gcc ctg agc aaa gac ccc aac gag aag cgc gat cac atg gtc ctg ctg	144
	Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu	
	35 40 45	
55	gag ttc gtg acc gcc gcc ggg atc act ctc ggc atg gac gag ctg tac	192
	Glu Phe Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr	
	50 55 60	
55	aag	195
	Lys	
	65	





	ggc gac ggc ccc gtg ctg ctg ccc gac aac cac tac ctg agc cac cag	96
	Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser His Gln	
	20 25 30	
5	tcc gcc ctg agc aaa gac ccc aac gag aag cgc gat cac atg gtc ctg	144
	Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu	
	35 40 45	
10	ctg gag ttc gtg acc gcc gcc ggg atc act ctc ggc atg gac gag ctg	192
	Leu Glu Phe Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu	
	50 55 60	
15	tac aag	198
	Tyr Lys	
	65	
20	Venus F2E, S175G mutation	
	SEQ ID NOS:876 & 877	
	ggc ggc gtg cag ctc gcc gac cac tac cag cag aac acc ccc atc ggc	48
	Gly Gly Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly	
	1 5 10 15	
25	gac ggc ccc gtg ctg ctg ccc gac aac cac tac ctg agc tac cag tcc	96
	Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Tyr Gln Ser	
	20 25 30	
30	gcc ctg agc aaa gac ccc aac gag aag cgc gat cac atg gtc ctg ctg	144
	Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu	
	35 40 45	
35	gag ttc gtg acc gcc gcc ggg atc act ctc ggc atg gac gag ctg tac	192
	Glu Phe Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr	
	50 55 60	
40	aag	195
	Lys	
	65	
45	Venus F2E, S175G mutation, Met added @ pos. 1	
	SEQ ID NOS:878 & 879	
	atg ggc ggc gtg cag ctc gcc gac cac tac cag cag aac acc ccc atc	48
	Met Gly Gly Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile	
	1 5 10 15	
50	ggc gac ggc ccc gtg ctg ctg ccc gac aac cac tac ctg agc tac cag	96
	Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Tyr Gln	
	20 25 30	
55	tcc gcc ctg agc aaa gac ccc aac gag aag cgc gat cac atg gtc ctg	144
	Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu	
	35 40 45	

	ctg gag ttc gtg acc gcc gcc ggg atc act ctc ggc atg gac gag ctg	192
	Leu Glu Phe Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu	
	50 55 60	
5	tac aag	198
	Tyr Lys	
	65	
10	Venus F2E, S175G,Y203T mutations	
	SEQ ID NOS:880 & 881	
	ggc ggc gtg cag ctc gcc gac cac tac cag cag aac acc ccc atc ggc	48
	Gly Gly Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly	
15	1 5 10 15	
	gac ggc ccc gtg ctg ctg ccc gac aac cac tac ctg agc acc cag tcc	96
	Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser	
	20 25 30	
20	gcc ctg agc aaa gac ccc aac gag aag cgc gat cac atg gtc ctg ctg	144
	Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu	
	35 40 45	
25	gag ttc gtg acc gcc gcc ggg atc act ctc ggc atg gac gag ctg tac	192
	Glu Phe Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr	
	50 55 60	
30	aag	195
	Lys	
	65	
35	Venus F2E, S175G, Y203T mutations, Met added @ pos. 1	
	SEQ ID NOS:882 & 883	
	atg ggc ggc gtg cag ctc gcc gac cac tac cag cag aac acc ccc atc	48
	Met Gly Gly Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile	
40	1 5 10 15	
	ggc gac ggc ccc gtg ctg ctg ccc gac aac cac tac ctg agc acc cag	96
	Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln	
	20 25 30	
45	tcc gcc ctg agc aaa gac ccc aac gag aag cgc gat cac atg gtc ctg	144
	Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu	
	35 40 45	
50	ctg gag ttc gtg acc gcc gcc ggg atc act ctc ggc atg gac gag ctg	192
	Leu Glu Phe Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu	
	50 55 60	
55	tac aag	198
	Tyr Lys	
	65	

Venus F2E, S175G, Y203F mutations  
SEQ ID NOS:884 & 885

5	ggc ggc gtg cag ctc gcc gac cac tac cag cag aac acc ccc atc ggc Gly Gly Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly 1 5 10 15	48	
10	gac ggc ccc gtg ctg ctg ccc gac aac cac tac ctg agc ttc cag tcc Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Phe Gln Ser 20 25 30	96	
15	gcc ctg agc aaa gac ccc aac gag aag cgc gat cac atg gtc ctg ctg Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu 35 40 45	144	
20	gag ttc gtg acc gcc gcc ggg atc act ctc ggc atg gac gag ctg tac Glu Phe Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr 50 55 60	192	
	aag Lys 65	195	
25	Venus F2E, S175G,Y203F mutations, Met added @ pos. 1 SEQ ID NOS:886 & 887		
30	atg ggc ggc gtg cag ctc gcc gac cac tac cag cag aac acc ccc atc Met Gly Gly Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile 1 5 10 15	48	
35	ggc gac ggc ccc gtg ctg ctg ccc gac aac cac tac ctg agc ttc cag Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Phe Gln 20 25 30	96	
40	tcc gcc ctg agc aaa gac ccc aac gag aag cgc gat cac atg gtc ctg Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu 35 40 45	144	
	ctg gag ttc gtg acc gcc gcc ggg atc act ctc ggc atg gac gag ctg Leu Glu Phe Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu 50 55 60	192	
45	tac aag Tyr Lys 65	198	
50	YFP F1F, position 1 Met removed (YFP F1F corresponds to aa residues 1-191 of YFP) SEQ ID NOS:888 & 889		
55	gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val 1 5 10 15	48	

	gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag	96
	Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu	
	20 25 30	
5	ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc tgc	144
	Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys	
	35 40 45	
10	acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ttc	192
	Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe	
	50 55 60	
15	ggc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag cgg	240
	Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg	
	65 70 75 80	
20	cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc	288
	His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg	
	85 90 95	
	acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag gtg	336
	Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val	
	100 105 110	
25	aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc atc	384
	Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile	
	115 120 125	
30	gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac	432
	Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn	
	130 135 140	
35	tac aac agc cac aac gtc tat atc atg gcc gac aag cag aag aac ggc	480
	Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly	
	145 150 155 160	
40	atc aag gtg aac ttc aag atc cgc cac aac atc gag gac ggc agc gtg	528
	Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val	
	165 170 175	
	cag ctc gcc gac cac tac cag cag aac acc ccc atc ggc gac	570
	Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp	
	180 185 190	
45	YFP F1F, K79R mutation SEQ ID NOS:890 & 891	
50	atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg	48
	Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu	
	1 5 10 15	
55	gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc	96
	Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly	
	20 25 30	

	gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc	144
	Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile	
	35 40 45	
5	tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc	192
	Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr	
	50 55 60	
10	ttc ggc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg cgc	240
	Phe Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Arg	
	65 70 75 80	
15	cgg cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag	288
	Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu	
	85 90 95	
20	cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag	336
	Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu	
	100 105 110	
25	gtg aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc	384
	Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly	
	115 120 125	
30	atc gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac	432
	Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr	
	130 135 140	
35	aac tac aac agc cac aac gtc tat atc atg gcc gac aag cag aag aac	480
	Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn	
	145 150 155 160	
40	ggc atc aag gtg aac ttc aag atc cgc cac aac atc gag gac ggc agc	528
	Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser	
	165 170 175	
45	gtg cag ctc gcc gac cac tac cag cag aac acc ccc atc ggc gac	573
	Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp	
	180 185 190	
YFP F1F, K79R mutation, pos. 1 Met removed		
SEQ ID NOS:892 & 893		
50	gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc	48
	Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val	
	1 5 10 15	
55	gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag	96
	Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu	
	20 25 30	
60	ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc tgc	144
	Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys	
	35 40 45	

	acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ttc	192
	Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe	
	50 55 60	
5	ggc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg cgc cgg	240
	Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Arg Arg	
	65 70 75 80	
10	cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc	288
	His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg	
	85 90 95	
15	acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag gtg	336
	Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val	
	100 105 110	
20	aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc atc	384
	Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile	
	115 120 125	
25	gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac	432
	Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn	
	130 135 140	
30	tac aac agc cac aac gtc tat atc atg gcc gac aag cag aag aac ggc	480
	Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly	
	145 150 155 160	
35	atc aag gtg aac ttc aag atc cgc cac aac atc gag gac ggc agc gtg	528
	Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val	
	165 170 175	
40	cag ctc gcc gac cac tac cag cag aac acc ccc atc ggc gac	570
	Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp	
	180 185 190	
40	YFP F1F, Y66F mutation	
	SEQ ID NOS:894 & 895	
45	atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg	48
	Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu	
	1 5 10 15	
50	gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc	96
	Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly	
	20 25 30	
55	gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc	144
	Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile	
	35 40 45	
55	tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc	192
	Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr	
	50 55 60	

	ttc ggc ttc ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag	240
	Phe Gly Phe Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys	
	65 70 75 80	
5	egg cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag	288
	Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu	
	85 90 95	
10	cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag	336
	Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu	
	100 105 110	
15	gtg aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc	384
	Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly	
	115 120 125	
20	atc gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac	432
	Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr	
	130 135 140	
25	aac tac aac agc cac aac gtc tat atc atg gcc gac aag cag aag aac	480
	Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn	
	145 150 155 160	
30	ggc atc aag gtg aac ttc aag atc cgc cac aac atc gag gac ggc agc	528
	Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser	
	165 170 175	
35	gtg cag ctc gcc gac cac tac cag cag aac acc ccc atc ggc gac	573
	Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp	
	180 185 190	
40	YFP F1F, Y66F mutation, pos. 1 Met removed	
	SEQ ID NOS:896 & 897	
40	gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc	48
	Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val	
	1 5 10 15	
45	gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag	96
	Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu	
	20 25 30	
50	ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc tgc	144
	Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys	
	35 40 45	
55	acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ttc	192
	Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe	
	50 55 60	
60	ggc ttc ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag cgg	240
	Gly Phe Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg	
	65 70 75 80	



	cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc	288
	His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg	
	85 90 95	
5	acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag gtg	336
	Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val	
	100 105 110	
10	aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc atc	384
	Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile	
	115 120 125	
15	gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac	432
	Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn	
	130 135 140	
20	tac aac agc cac aac gtc tat atc atg gcc gac aag cag aag aac ggc	480
	Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly	
	145 150 155 160	
	atc aag gtg aac ttc aag atc cgc cac aac atc gag gac ggc agc gtg	528
	Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val	
	165 170 175	
25	cag ctc gcc gac cac tac cag cag aac acc ccc atc ggc gac	570
	Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp	
	180 185 190	
30	YFP F1F, Q69K mutation SEQ ID NOS:898 & 899	
35	atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg	48
	Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu	
	1 5 10 15	
40	gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc	96
	Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly	
	20 25 30	
45	gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc	144
	Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile	
	35 40 45	
	tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc	192
	Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr	
	50 55 60	
50	ttc ggc tac ggc ctg aag tgc ttc gcc cgc tac ccc gac cac atg aag	240
	Phe Gly Tyr Gly Leu Lys Cys Phe Ala Arg Tyr Pro Asp His Met Lys	
	65 70 75 80	
55	cgg cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag	288
	Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu	
	85 90 95	

	cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag	336
	Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu	
	100 105 110	
5	gtg aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc	384
	Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly	
	115 120 125	
10	atc gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac	432
	Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr	
	130 135 140	
15	aac tac aac agc cac aac gtc tat atc atg gcc gac aag cag aag aac	480
	Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn	
	145 150 155 160	
20	ggc atc aag gtg aac ttc aag atc cgc cac aac atc gag gac ggc agc	528
	Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser	
	165 170 175	
25	gtg cag ctc gcc gac cac tac cag cag aac acc ccc atc ggc gac	573
	Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp	
	180 185 190	
30	gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc	48
	Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val	
	1 5 10 15	
35	gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag	96
	Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu	
	20 25 30	
40	ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc tgc	144
	Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys	
	35 40 45	
45	acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ttc	192
	Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe	
	50 55 60	
50	ggc tac ggc ctg aag tgc ttc gcc cgc tac ccc gac cac atg aag cgg	240
	Gly Tyr Gly Leu Lys Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg	
	65 70 75 80	
55	cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc	288
	His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg	
	85 90 95	
60	acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag gtg	336
	Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val	
	100 105 110	

YFP F1F, Q69K mutation, pos. 1 Met removed  
SEQ ID NOS:900 & 901

	aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc atc	384
	Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile	
	115 120 125	
5	gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac	432
	Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn	
	130 135 140	
10	tac aac agc cac aac gtc tat atc atg gcc gac aag cag aag aac ggc	480
	Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly	
	145 150 155 160	
15	atc aag gtg aac ttc aag atc cgc cac aac atc gag gac ggc agc gtg	528
	Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val	
	165 170 175	
20	cag ctc gcc gac cac tac cag cag aac acc ccc atc ggc gac	570
	Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp	
	180 185 190	
	citrine F1F,V68L,Q69M mutations	
	SEQ ID NOS:902 & 903	
25	atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg	48
	Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu	
	1 5 10 15	
30	gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc	96
	Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly	
	20 25 30	
35	gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc	144
	Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile	
	35 40 45	
40	tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc	192
	Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr	
	50 55 60	
45	ttc ggc tac ggc ctg atg tgc ttc gcc cgc tac ccc gac cac atg aag	240
	Phe Gly Tyr Gly Leu Met Cys Phe Ala Arg Tyr Pro Asp His Met Lys	
	65 70 75 80	
	cgg cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag	288
	Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu	
	85 90 95	
50	cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag	336
	Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu	
	100 105 110	
55	gtg aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc	384
	Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly	
	115 120 125	

	atc gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac	432
	Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr	
	130 135 140	
5	aac tac aac agc cac aac gtc tat atc atg gcc gac aag cag aag aac	480
	Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn	
	145 150 155 160	
10	ggc atc aag gtg aac ttc aag atc cgc cac aac atc gag gac ggc agc	528
	Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser	
	165 170 175	
15	gtg cag ctc gcc gac cac tac cag cag aac acc ccc atc ggc gac	573
	Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp	
	180 185 190	
20	citrine F1F, V68L,Q69M mutations, pos. 1 Met removed	
	SEQ ID NOS:904 & 905	
	gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc	48
	Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val	
	1 5 10 15	
25	gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag	96
	Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu	
	20 25 30	
30	ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc tgc	144
	Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys	
	35 40 45	
35	acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ttc	192
	Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe	
	50 55 60	
40	ggc tac ggc ctg atg tgc ttc gcc cgc tac ccc gac cac atg aag cgg	240
	Gly Tyr Gly Leu Met Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg	
	65 70 75 80	
45	cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc	288
	His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg	
	85 90 95	
	acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag gtg	336
	Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val	
	100 105 110	
50	aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc atc	384
	Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile	
	115 120 125	
55	gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac	432
	Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn	
	130 135 140	

	tac aac agc cac aac gtc tat atc atg gcc gac aag cag aag aac ggc	480
	Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly	
	145 150 155 160	
5	atc aag gtg aac ttc aag atc cgc cac aac atc gag gac ggc agc gtg	528
	Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val	
	165 170 175	
10	cag ctg gcc gac cac tac cag cag aac acc ccc atc ggc gac	570
	Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp	
	180 185 190	
15	CFP F1F, F64L mutation	
	SEQ ID NOS:906 & 907	
20	atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg	48
	Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu	
	1 5 10 15	
25	gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc	96
	Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly	
	20 25 30	
30	gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc	144
	Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile	
	35 40 45	
35	tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctg gtg acc acc	192
	Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr	
	50 55 60	
40	ctg ggc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag	240
	Leu Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys	
	65 70 75 80	
45	cgg cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag	288
	Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu	
	85 90 95	
50	cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag	336
	Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu	
	100 105 110	
55	gtg aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc	384
	Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly	
	115 120 125	
60	atc gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac	432
	Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr	
	130 135 140	
65	aac tac aac agc cac aac gtc tat atc atg gcc gac aag cag aag aac	480
	Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn	
	145 150 155 160	

	ggc atc aag gtg aac ttc aag atc cgc cac aac atc gag gac ggc agc	528
	Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser	
	165 170 175	
5	gtg cag ctc gcc gac cac tac cag cag aac acc ccc atc ggc gac	573
	Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp	
	180 185 190	
10	CFP F1F, F64L mutation, pos. 1 Met removed SEQ ID NOS:908 & 909	
15	gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc	48
	Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val	
	1 5 10 15	
20	gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag	96
	Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu	
	20 25 30	
25	ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc tgc	144
	Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys	
	35 40 45	
30	acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ctg	192
	Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Leu	
	50 55 60	
35	ggc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag cgg	240
	Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg	
	65 70 75 80	
35	cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc	288
	His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg	
	85 90 95	
40	acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag gtg	336
	Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val	
	100 105 110	
45	aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc atc	384
	Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile	
	115 120 125	
50	gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac	432
	Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn	
	130 135 140	
50	tac aac agc cac aac gtc tat atc atg gcc gac aag cag aag aac ggc	480
	Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly	
	145 150 155 160	
55	atc aag gtg aac ttc aag atc cgc cac aac atc gag gac ggc agc gtg	528
	Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val	
	165 170 175	

cag	ctc	gcc	gac	cac	tac	cag	cag	aac	acc	ccc	atc	ggc	gac	570
Gln	Leu	Ala	Asp	His	Tyr	Gln	Gln	Asn	Thr	Pro	Ile	Gly	Asp	
			180					185					190	

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CFP F1F, F64L, S65T, Y66W mutations  
SEQ ID NOS:910 & 911

10	atg	gtg	agc	aag	ggc	gag	gag	ctg	ttc	acc	ggg	gtg	gtg	ccc	atc	ctg	48
	Met	Val	Ser	Lys	Gly	Glu	Glu	Leu	Phe	Thr	Gly	Val	Val	Pro	Ile	Leu	
	1				5				10					15			

15	gtc	gag	ctg	gac	ggc	gac	gta	aac	ggc	cac	aag	ttc	agc	gtg	tcc	ggc	96
	Val	Glu	Leu	Asp	Gly	Asp	Val	Asn	Gly	His	Lys	Phe	Ser	Val	Ser	Gly	
				20				25						30			

20	gag	ggc	gag	ggc	gat	gcc	acc	tac	ggc	aag	ctg	acc	ctg	aag	ttc	atc	144
	Glu	Gly	Glu	Gly	Asp	Ala	Thr	Tyr	Gly	Lys	Leu	Thr	Leu	Lys	Phe	Ile	
			35					40					45				

25	tgc	acc	acc	ggc	aag	ctg	ccc	gtg	ccc	tgg	ccc	acc	ctc	gtg	acc	acc	192
	Cys	Thr	Thr	Gly	Lys	Leu	Pro	Val	Pro	Trp	Pro	Thr	Leu	Val	Thr	Thr	
		50					55					60					

30	ctg	acc	tgg	ggc	ctg	cag	tgc	ttc	gcc	cgc	tac	ccc	gac	cac	atg	aag	240
	Leu	Thr	Trp	Gly	Leu	Gln	Cys	Phe	Ala	Arg	Tyr	Pro	Asp	His	Met	Lys	
	65				70				75						80		

30	cgg	cac	gac	ttc	ttc	aag	tcc	gcc	atg	ccc	gaa	ggc	tac	gtc	cag	gag	288
	Arg	His	Asp	Phe	Phe	Lys	Ser	Ala	Met	Pro	Glu	Gly	Tyr	Val	Gln	Glu	
				85					90					95			

35	cgc	acc	atc	ttc	ttc	aag	gac	gac	ggc	aac	tac	aag	acc	cgc	gcc	gag	336
	Arg	Thr	Ile	Phe	Phe	Lys	Asp	Asp	Gly	Asn	Tyr	Lys	Thr	Arg	Ala	Glu	
			100					105					110				

40	gtg	aag	ttc	gag	ggc	gac	acc	ctg	gtg	aac	cgc	atc	gag	ctg	aag	ggc	384
	Val	Lys	Phe	Glu	Gly	Asp	Thr	Leu	Val	Asn	Arg	Ile	Glu	Leu	Lys	Gly	
			115					120					125				

45	atc	gac	ttc	aag	gag	gac	ggc	aac	atc	ctg	ggg	cac	aag	ctg	gag	tac	432
	Ile	Asp	Phe	Lys	Glu	Asp	Gly	Asn	Ile	Leu	Gly	His	Lys	Leu	Glu	Tyr	
			130				135					140					

50	aac	tac	aac	agc	cac	aac	gtc	tat	atc	atg	gcc	gac	aag	cag	aag	aac	480
	Asn	Tyr	Asn	Ser	His	Asn	Val	Tyr	Ile	Met	Ala	Asp	Lys	Gln	Lys	Asn	
	145					150					155				160		

50	ggc	atc	aag	gtg	aac	ttc	aag	atc	cgc	cac	aac	atc	gag	gac	ggc	agc	528
	Gly	Ile	Lys	Val	Asn	Phe	Lys	Ile	Arg	His	Asn	Ile	Glu	Asp	Gly	Ser	
				165					170						175		

55	gtg	cag	ctc	gcc	gac	cac	tac	cag	cag	aac	acc	ccc	atc	ggc	gac	573
	Val	Gln	Leu	Ala	Asp	His	Tyr	Gln	Gln	Asn	Thr	Pro	Ile	Gly	Asp	
				180				185							190	

CFP F1F, F64L,S65T,Y66W mutations, pos. 1 Met removed  
SEQ ID NOS:912 & 913

5	gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val 1 5 10 15	48
10	gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu 20 25 30	96
15	ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc tgc Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys 35 40 45	144
20	acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ctg Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Leu 50 55 60	192
25	acc tgg ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag cgg Thr Trp Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg 65 70 75 80	240
30	cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg 85 90 95	288
35	acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag gtg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val 100 105 110	336
40	aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc atc Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile 115 120 125	384
45	gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn 130 135 140	432
50	tac aac agc cac aac gtc tat atc atg gcc gac aag cag aag aac ggc Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly 145 150 155 160	480
55	atc aag gtg aac ttc aag atc cgc cac aac atc gag gac ggc agc gtg Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val 165 170 175	528
60	cag ctc gcc gac cac tac cag cag aac acc ccc atc ggc gac Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp 180 185 190	570



CFP F1F, F64L,S65T,Y66W,N146I,M153T,V163A mutations  
SEQ ID NOS:914 & 915

5	atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu	48
	1 5 10 15	
10	gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly	96
	20 25 30	
15	gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile	144
	35 40 45	
20	tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr	192
	50 55 60	
25	ctg acc tgg ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag Leu Thr Trp Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys	240
	65 70 75 80	
30	cgg cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu	288
	85 90 95	
35	cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu	336
	100 105 110	
40	gtg aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly	384
	115 120 125	
45	atc gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr	432
	130 135 140	
50	aac tac atc agc cac aac gtc tat atc acc gcc gac aag cag aag aac Asn Tyr Ile Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn	480
	145 150 155 160	
55	ggc atc aag gcc aac ttc aag atc cgc cac aac atc gag gac ggc agc Gly Ile Lys Ala Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser	528
	165 170 175	
60	gtg cag ctc gcc gac cac tac cag cag aac acc ccc atc ggc gac Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp	576
	180 185 190	

CFP F1F, F64L, S65T, Y66W, N146I, M153T, V163A mutations, pos. 1 Met removed  
SEQ ID NOS:916 & 917

5	gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val 1 5 10 15	48
10	gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu 20 25 30	96
15	ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc tgc Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys 35 40 45	144
20	acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ctg Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Leu 50 55 60	192
25	acc tgg ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag cgg Thr Trp Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg 65 70 75 80	240
30	cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg 85 90 95	288
35	acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag gtg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val 100 105 110	336
40	aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc atc Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile 115 120 125	384
45	gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn 130 135 140	432
50	tac atc agc cac aac gtc tat atc acc gcc gac aag cag aag aac ggc Tyr Ile Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly 145 150 155 160	480
55	atc aag gcc aac ttc aag atc cgc cac aac atc gag gac ggc agc gtg Ile Lys Ala Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val 165 170 175	528
60	cag ctc gcc gac cac tac cag cag aac acc ccc atc ggc gac Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp 180 185 190	570

CFP F1F, Y66W mutation  
SEQ ID NOS:918 & 919

5	atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu 1 5 10 15	48
10	gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly 20 25 30	96
15	gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile 35 40 45	144
20	tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr 50 55 60	192
25	ttc ggc tgg ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag Phe Gly Trp Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys 65 70 75 80	240
30	cgg cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu 85 90 95	288
35	cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu 100 105 110	336
40	gtg aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly 115 120 125	384
45	atc gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr 130 135 140	432
50	aac tac aac agc cac aac gtc tat atc atg gcc gac aag cag aag aac Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn 145 150 155 160	480
55	ggc atc aag gtg aac ttc aag atc cgc cac aac atc gag gac ggc agc Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser 165 170 175	528
60	gtg cag ctc gcc gac cac tac cag cag aac acc ccc atc ggc gac Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp 180 185 190	573

CFP F1F, Y66W mutation, pos. 1 Met removed  
SEQ ID NOS:920 & 921

5	gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val 1 5 10 15	48
10	gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu 20 25 30	96
15	ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc tgc Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys 35 40 45	144
20	acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ttc Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe 50 55 60	192
25	ggc tgg ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag cgg Gly Trp Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg 65 70 75 80	240
30	cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg 85 90 95	288
35	acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag gtg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val 100 105 110	336
40	aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc atc Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile 115 120 125	384
45	gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn 130 135 140	432
50	tac aac agc cac aac gtc tat atc atg gcc gac aag cag aag aac ggc Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly 145 150 155 160	480
55	atc aag gtg aac ttc aag atc cgc cac aac atc gag gac ggc agc gtg Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val 165 170 175	528
60	cag ctc gcc gac cac tac cag cag aac acc ccc atc ggc gac Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp 180 185 190	570

CFP F1F, Y66W, N146I mutations  
SEQ ID NOS:922 & 923

5	atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu 1 5 10 15	48
10	gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly 20 25 30	96
15	gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile 35 40 45	144
20	tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr 50 55 60	192
25	ttc ggc tgg ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag Phe Gly Trp Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys 65 70 75 80	240
30	cgg cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu 85 90 95	288
35	cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu 100 105 110	336
40	gtg aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly 115 120 125	384
45	atc gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr 130 135 140	432
50	aac tac atc agc cac aac gtc tat atc atg gcc gac aag cag aag aac Asn Tyr Ile Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn 145 150 155 160	480
55	ggc atc aag gtg aac ttc aag atc cgc cac aac atc gag gac ggc agc Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser 165 170 175	528
60	gtg cag ctc gcc gac cac tac cag cag aac acc ccc atc ggc gac Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp 180 185 190	576

CFP F1F, Y66W, N146I mutations, pos. 1 Met removed  
SEQ ID NOS:924 & 925

55	gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val	48
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	1			5					10					15			
	gag	ctg	gac	ggc	gac	gta	aac	ggc	cac	aag	ttc	agc	gtg	tcc	ggc	gag	96
5	Glu	Leu	Asp	Gly	Asp	Val	Asn	Gly	His	Lys	Phe	Ser	Val	Ser	Gly	Glu	
				20					25					30			
	ggc	gag	ggc	gat	gcc	acc	tac	ggc	aag	ctg	acc	ctg	aag	ttc	atc	tgc	144
	Gly	Glu	Gly	Asp	Ala	Thr	Tyr	Gly	Lys	Leu	Thr	Leu	Lys	Phe	Ile	Cys	
				35				40					45				
10	acc	acc	ggc	aag	ctg	ccc	gtg	ccc	tgg	ccc	acc	ctc	gtg	acc	acc	ttc	192
	Thr	Thr	Gly	Lys	Leu	Pro	Val	Pro	Trp	Pro	Thr	Leu	Val	Thr	Thr	Phe	
				50			55					60					
15	ggc	tgg	ggc	ctg	cag	tgc	ttc	gcc	cgc	tac	ccc	gac	cac	atg	aag	cgg	240
	Gly	Trp	Gly	Leu	Gln	Cys	Phe	Ala	Arg	Tyr	Pro	Asp	His	Met	Lys	Arg	
	65				70				75						80		
20	cac	gac	ttc	ttc	aag	tcc	gcc	atg	ccc	gaa	ggc	tac	gtc	cag	gag	cgc	288
	His	Asp	Phe	Phe	Lys	Ser	Ala	Met	Pro	Glu	Gly	Tyr	Val	Gln	Glu	Arg	
					85				90					95			
	acc	atc	ttc	ttc	aag	gac	gac	ggc	aac	tac	aag	acc	cgc	gcc	gag	gtg	336
25	Thr	Ile	Phe	Phe	Lys	Asp	Asp	Gly	Asn	Tyr	Lys	Thr	Arg	Ala	Glu	Val	
				100				105					110				
	aag	ttc	gag	ggc	gac	acc	ctg	gtg	aac	cgc	atc	gag	ctg	aag	ggc	atc	384
	Lys	Phe	Glu	Gly	Asp	Thr	Leu	Val	Asn	Arg	Ile	Glu	Leu	Lys	Gly	Ile	
			115				120					125					
30	gac	ttc	aag	gag	gac	ggc	aac	atc	ctg	ggg	cac	aag	ctg	gag	tac	aac	432
	Asp	Phe	Lys	Glu	Asp	Gly	Asn	Ile	Leu	Gly	His	Lys	Leu	Glu	Tyr	Asn	
			130				135					140					
35	tac	atc	agc	cac	aac	gtc	tat	atc	atg	gcc	gac	aag	cag	aag	aac	ggc	480
	Tyr	Ile	Ser	His	Asn	Val	Tyr	Ile	Met	Ala	Asp	Lys	Gln	Lys	Asn	Gly	
	145				150				155						160		
40	atc	aag	gtg	aac	ttc	aag	atc	cgc	cac	aac	atc	gag	gac	ggc	agc	gtg	528
	Ile	Lys	Val	Asn	Phe	Lys	Ile	Arg	His	Asn	Ile	Glu	Asp	Gly	Ser	Val	
				165				170						175			
	cag	ctc	gcc	gac	cac	tac	cag	cag	aac	acc	ccc	atc	ggc	gac			570
45	Gln	Leu	Ala	Asp	His	Tyr	Gln	Gln	Asn	Thr	Pro	Ile	Gly	Asp			
			180					185					190				
	CFP F1F, M153T mutation																
50	SEQ ID NOS:926 & 927																
	atg	gtg	agc	aag	ggc	gag	gag	ctg	ttc	acc	ggg	gtg	gtg	ccc	atc	ctg	48
	Met	Val	Ser	Lys	Gly	Glu	Glu	Leu	Phe	Thr	Gly	Val	Val	Pro	Ile	Leu	
	1				5				10				15				
55	gtc	gag	ctg	gac	ggc	gac	gta	aac	ggc	cac	aag	ttc	agc	gtg	tcc	ggc	96
	Val	Glu	Leu	Asp	Gly	Asp	Val	Asn	Gly	His	Lys	Phe	Ser	Val	Ser	Gly	
			20					25					30				

	gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc	144														
	Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile															
	35 40 45															
5	tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc	192														
	Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr															
	50 55 60															
10	ttc ggc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag	240														
	Phe Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys															
	65 70 75 80															
15	cgg cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag	288														
	Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu															
	85 90 95															
20	cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag	336														
	Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu															
	100 105 110															
25	gtg aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc	384														
	Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly															
	115 120 125															
30	atc gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac	432														
	Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr															
	130 135 140															
35	aac tac aac agc cac aac gtc tat atc acc gcc gac aag cag aag aac	480														
	Asn Tyr Asn Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn															
	145 150 155 160															
40	ggc atc aag gtg aac ttc aag atc cgc cac aac atc gag gac ggc agc	528														
	Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser															
	165 170 175															
45	gtg cag ctc gcc gac cac tac cag cag aac acc ccc atc ggc gac	573														
	Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp															
	180 185 190															
	CFP F1F, M153T mutation, pos. 1 Met removed															
	SEQ ID NOS:928 & 929															
50	gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc	48														
	Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val															
	1 5 10 15															
55	gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag	96														
	Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu															
	20 25 30															
60	ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc tgc	144														
	Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys															
	35 40 45															

	acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ttc	192
	Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe	
	50 55 60	
5	ggc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag cgg	240
	Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg	
	65 70 75 80	
10	cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc	288
	His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg	
	85 90 95	
15	acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag gtg	336
	Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val	
	100 105 110	
20	aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc atc	384
	Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile	
	115 120 125	
25	gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac	432
	Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn	
	130 135 140	
30	tac aac agc cac aac gtc tat atc acc gcc gac aag cag aag aac ggc	480
	Tyr Asn Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly	
	145 150 155 160	
35	atc aag gtg aac ttc aag atc cgc cac aac atc gag gac ggc agc gtg	528
	Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val	
	165 170 175	
40	cag ctc gcc gac cac tac cag cag aac acc ccc atc ggc gac	570
	Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp	
	180 185 190	
45	CFP F1F, M153T mutation	
	SEQ ID NOS:930 & 931	
50	atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg	48
	Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu	
	1 5 10 15	
55	gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc	96
	Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly	
	20 25 30	
60	gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc	144
	Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile	
	35 40 45	
65	tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc	192
	Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr	
	50 55 60	



	ttc ggc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag	240
	Phe Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys	
	65 70 75 80	
5	cgg cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag	288
	Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu	
	85 90 95	
10	cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag	336
	Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu	
	100 105 110	
15	gtg aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc	384
	Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly	
	115 120 125	
20	atc gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac	432
	Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr	
	130 135 140	
25	aac tac atc agc cac aac gtc tat atc acc gcc gac aag cag aag aac	480
	Asn Tyr Ile Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn	
	145 150 155 160	
30	ggc atc aag gtg aac ttc aag atc cgc cac aac atc gag gac ggc agc	528
	Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser	
	165 170 175	
35	gtg cag ctc gcc gac cac tac cag cag aac acc ccc atc ggc gac	573
	Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp	
	180 185 190	
35	CFP F1F, N146I,M153T mutations, pos. 1 Met removed	
	SEQ ID NOS:932 & 933	
40	gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc	48
	Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val	
	1 5 10 15	
45	gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag	96
	Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu	
	20 25 30	
50	ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc tgc	144
	Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys	
	35 40 45	
55	acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ttc	192
	Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe	
	50 55 60	
55	ggc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag cgg	240
	Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg	
	65 70 75 80	

	cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc	288
	His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg	
	85 90 95	
5	acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag gtg	336
	Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val	
	100 105 110	
10	aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc atc	384
	Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile	
	115 120 125	
15	gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac	432
	Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn	
	130 135 140	
20	tac atc agc cac aac gtc tat atc acc gcc gac aag cag aag aac ggc	480
	Tyr Ile Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly	
	145 150 155 160	
	atc aag gtg aac ttc aag atc cgc cac aac atc gag gac ggc agc gtg	528
	Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val	
	165 170 175	
25	cag ctc gcc gac cac tac cag cag aac acc ccc atc ggc gac	570
	Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp	
	180 185 190	
30	CFP F1F, N146I, M153T, V163A mutations	
	SEQ ID NOS:934 & 935	
35	atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg	48
	Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu	
	1 5 10 15	
40	gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc	96
	Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly	
	20 25 30	
	gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc	144
	Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile	
	35 40 45	
45	tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc	192
	Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr	
	50 55 60	
50	ttc ggc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag	240
	Phe Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys	
	65 70 75 80	
55	cgg cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag	288
	Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu	
	85 90 95	

	cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag	336
	Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu	
	100 105 110	
5	gtg aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc	384
	Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly	
	115 120 125	
10	atc gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac	432
	Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr	
	130 135 140	
15	aac tac atc agc cac aac gtc tat atc acc gcc gac aag cag aag aac	480
	Asn Tyr Ile Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn	
	145 150 155 160	
20	ggc atc aag gcc aac ttc aag atc cgc cac aac atc gag gac ggc agc	528
	Gly Ile Lys Ala Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser	
	165 170 175	
25	gtg cag ctc gcc gac cac tac cag cag aac acc ccc atc ggc gac	573
	Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp	
	180 185 190	
30	CFP F1F, N146I,M153T,V163A mutations, pos. 1 Met removed	
	SEQ ID NOS:936 & 937	
30	gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc	48
	Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val	
	1 5 10 15	
35	gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag	96
	Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu	
	20 25 30	
40	ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc tgc	144
	Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys	
	35 40 45	
45	acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ttc	192
	Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe	
	50 55 60	
50	ggc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag cgg	240
	Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg	
	65 70 75 80	
55	cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc	288
	His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg	
	85 90 95	
55	acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag gtg	336
	Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val	
	100 105 110	

	aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc atc Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile 115 120 125	384	
5	gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn 130 135 140	432	
10	tac atc agc cac aac gtc tat atc acc gcc gac aag cag aag aac ggc Tyr Ile Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly 145 150 155 160	480	
15	atc aag gcc aac ttc aag atc cgc cac aac atc gag gac ggc agc gtg Ile Lys Ala Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val 165 170 175	528	
20	cag ctc gcc gac cac tac cag cag aac acc ccc atc ggc gac Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp 180 185 190	570	
25	CFP F1F, Y66W,N146I,M153T mutations SEQ ID NOS:938 & 939		
30	atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu 1 5 10 15	48	
35	gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly 20 25 30	96	
40	gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile 35 40 45	144	
45	tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr 50 55 60	192	
50	ttc ggc tgg ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag Phe Gly Trp Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys 65 70 75 80	240	
55	cgg cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu 85 90 95	288	
60	cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu 100 105 110	336	
65	gtg aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly 115 120 125	384	

	atc gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac	432
	Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr	
	130 135 140	
5	aac tac atc agc cac aac gtc tat atc acc gcc gac aag cag aag aac	480
	Asn Tyr Ile Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn	
	145 150 155 160	
10	ggc atc aag gtg aac ttc aag atc cgc cac aac atc gag gac ggc agc	528
	Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser	
	165 170 175	
15	gtg cag ctg gcc gac cac tac cag cag aac acc ccc atc ggc gac	573
	Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp	
	180 185 190	
20	CFP F1F, Y66W,N146I,M153T mutations, pos. 1 Met removed	
	SEQ ID NOS:940 & 941	
25	gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc	48
	Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val	
	1 5 10 15	
30	gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag	96
	Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu	
	20 25 30	
35	ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc tgc	144
	Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys	
	35 40 45	
40	acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ttc	192
	Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe	
	50 55 60	
45	ggc tgg ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag cgg	240
	Gly Trp Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg	
	65 70 75 80	
50	cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc	288
	His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg	
	85 90 95	
55	acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag gtg	336
	Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val	
	100 105 110	
60	aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc atc	384
	Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile	
	115 120 125	
65	gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac	432
	Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn	
	130 135 140	

	tac atc agc cac aac gtc tat atc acc gcc gac aag cag aag aac ggc	480
	Tyr Ile Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly	
	145 150 155 160	
5	atc aag gtg aac ttc aag atc cgc cac aac atc gag gac ggc agc gtg	528
	Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val	
	165 170 175	
10	cag ctc gcc gac cac tac cag cag aac acc ccc atc ggc gac	570
	Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp	
	180 185 190	
15	CFP F1F, Y66W, N146I, M153T, V163A mutations SEQ ID NOS:942 & 943	
20	atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg	48
	Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu	
	1 5 10 15	
25	gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc	96
	Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly	
	20 25 30	
30	gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc	144
	Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile	
	35 40 45	
35	tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc	192
	Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr	
	50 55 60	
40	ttc ggc tgg ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag	240
	Phe Gly Trp Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys	
	65 70 75 80	
45	cgg cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag	288
	Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu	
	85 90 95	
50	cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag	336
	Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu	
	100 105 110	
55	gtg aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc	384
	Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly	
	115 120 125	
60	atc gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac	432
	Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr	
	130 135 140	
65	aac tac atc agc cac aac gtc tat atc acc gcc gac aag cag aag aac	480
	Asn Tyr Ile Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn	
	145 150 155 160	

	ggc atc aag gcc aac ttc aag atc cgc cac aac atc gag gac ggc agc	528
	Gly Ile Lys Ala Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser	
	165 170 175	
5	gtg cag ctc gcc gac cac tac cag cag aac acc ccc atc ggc gac	573
	Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp	
	180 185 190	
10	CFP F1F, Y66W, N146I, M153T, V163A mutations, pos. 1 Met removed SEQ ID NOS:944 & 945	
15	gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc	48
	Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val	
	1 5 10 15	
20	gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag	96
	Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu	
	20 25 30	
25	ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc tgc	144
	Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys	
	35 40 45	
30	acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ttc	192
	Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe	
	50 55 60	
35	ggc tgg ggc ctg cag tgc ttc gcc cgc tac ccc gag cac atg aag cgg	240
	Gly Trp Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg	
	65 70 75 80	
40	cac gag ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc	288
	His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg	
	85 90 95	
45	acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag gtg	336
	Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val	
	100 105 110	
50	aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc atc	384
	Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile	
	115 120 125	
55	gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac	432
	Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn	
	130 135 140	
60	tac atc agc cac aac gtc tat atc acc gcc gag aag cag aag aac ggc	480
	Tyr Ile Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly	
	145 150 155 160	
65	atc aag gcc aac ttc aag atc cgc cac aac atc gag gac ggc agc gtg	528
	Ile Lys Ala Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val	
	165 170 175	

	cag ctc gcc gac cac tac cag cag aac acc ccc atc ggc gac	570
	Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp	
	180 185 190	
5	CFP F1F, S65A mutation SEQ ID NOS:946 & 947	
10	atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg	48
	Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu	
	1 5 10 15	
15	gtc gag ctg gac ggc gag gta aac ggc cac aag ttc agc gtg tcc ggc	96
	Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly	
	20 25 30	
20	gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc	144
	Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile	
	35 40 45	
25	tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc	192
	Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr	
	50 55 60	
30	ttc gcc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag	240
	Phe Ala Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys	
	65 70 75 80	
35	cgg cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag	288
	Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu	
	85 90 95	
40	cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag	336
	Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu	
	100 105 110	
45	gtg aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc	384
	Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly	
	115 120 125	
50	atc gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac	432
	Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr	
	130 135 140	
55	aac tac aac agc cac aac gtc tat atc atg gcc gac aag cag aag aac	480
	Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn	
	145 150 155 160	
60	ggc atc aag gtg aac ttc aag atc cgc cac aac atc gag gac ggc agc	528
	Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser	
	165 170 175	
65	gtg cag ctc gcc gac cac tac cag cag aac acc ccc atc ggc gac	573
	Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp	
	180 185 190	



CFP F1F, S65A mutation, pos. 1 Met removed  
SEQ ID NOS:948 & 949

5	gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val 1 5 10 15	48
10	gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu 20 25 30	96
15	ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc tgc Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys 35 40 45	144
20	acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ttc Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe 50 55 60	192
25	gcc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag cgg Ala Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg 65 70 75 80	240
30	cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg 85 90 95	288
35	acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag gtg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val 100 105 110	336
40	aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc atc Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile 115 120 125	384
45	gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn 130 135 140	432
50	tac aac agc cac aac gtc tat atc atg gcc gac aag cag aag aac ggc Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly 145 150 155 160	480
55	atc aag gtg aac ttc aag atc cgc cac aac atc gag gac ggc agc gtg Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val 165 170 175	528
60	cag ctc gcc gac cac tac cag cag aac acc ccc atc ggc gac Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp 180 185 190	576

CFP F1F, S65A, Y66W, S72A mutations  
SEQ ID NOS:950 & 951

5	atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu 1 5 10 15	48
10	gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly 20 25 30	96
15	gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile 35 40 45	144
20	tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr 50 55 60	192
25	ttc gcc tgg ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag Phe Ala Trp Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys 65 70 75 80	240
30	cgg cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu 85 90 95	288
35	cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu 100 105 110	336
40	gtg aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly 115 120 125	384
45	atc gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr 130 135 140	432
50	aac tac aac agc cac aac gtc tat atc atg gcc gac aag cag aag aac Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn 145 150 155 160	480
55	ggc atc aag gtg aac ttc aag atc cgc cac aac atc gag gac ggc agc Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser 165 170 175	528
60	gtg cag ctc gcc gac cac tac cag cag aac acc ccc atc ggc gac Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp 180 185 190	573

CFP F1F, S65A, Y66W, S72A mutations, pos. 1 Met removed  
 SEQ ID NOS:952 & 953

5	gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val 1 5 10 15	48
10	gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu 20 25 30	96
15	ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc tgc Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys 35 40 45	144
20	acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ttc Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe 50 55 60	192
25	gcc tgg ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag cgg Ala Trp Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg 65 70 75 80	240
30	cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg 85 90 95	288
35	acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag gtg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val 100 105 110	336
40	aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc atc Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile 115 120 125	384
45	gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn 130 135 140	432
50	tac aac agc cac aac gtc tat atc atg gcc gac aag cag aag aac ggc Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly 145 150 155 160	480
55	atc aag gtg aac ttc aag atc cgc cac aac atc gag gac ggc agc gtg Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val 165 170 175	528
60	cag ctc gcc gac cac tac cag cag aac acc ccc atc ggc gac Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp 180 185 190	570

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55

CFP F1F, S65A, Y66W, S72A, N146I, M153T, V163A mutations  
SEQ ID NOS:954 & 955

5	atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu 1 5 10 15	48
10	gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly 20 25 30	96
15	gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile 35 40 45	144
20	tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr 50 55 60	192
25	ttc gcc tgg ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag Phe Ala Trp Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys 65 70 75 80	240
30	cgg cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu 85 90 95	288
35	cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu 100 105 110	336
40	gtg aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly 115 120 125	384
45	atc gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr 130 135 140	432
50	aac tac atc agc cac aac gtc tat atc acc gcc gac aag cag aag aac Asn Tyr Ile Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn 145 150 155 160	480
55	ggc atc aag gcc aac ttc aag atc cgc cac aac atc gag gac ggc agc Gly Ile Lys Ala Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser 165 170 175	528
60	gtg cag ctc gcc gac cac tac cag cag aac acc ccc atc ggc gac Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp 180 185 190	573

CFP F1F, S65A, Y66W, S72A, N146I, M153T, V163A mutations, pos. 1  
Met removed  
SEQ ID NOS:956 & 957

5	gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val 1 5 10 15	48
10	gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu 20 25 30	96
15	ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc tgc Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys 35 40 45	144
20	acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ttc Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe 50 55 60	192
25	gcc tgg ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag cgg Ala Trp Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg 65 70 75 80	240
30	cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg 85 90 95	288
35	acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag gtg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val 100 105 110	336
40	aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc atc Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile 115 120 125	384
45	gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn 130 135 140	432
50	tac atc agc cac aac gtc tat atc acc gcc gac aag cag aag aac ggc Tyr Ile Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly 145 150 155 160	480
55	atc aag gcc aac ttc aag atc cgc cac aac atc gag gac ggc agc gtg Ile Lys Ala Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val 165 170 175	528
60	cag ctc gcc gac cac tac cag cag aac acc ccc atc ggc gac Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp 180 185 190	576

BFP F1F, Y66H mutation  
SEQ ID NOS:958 & 959

5	atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu 1 5 10 15	48
10	gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly 20 25 30	96
15	gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile 35 40 45	144
20	tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr 50 55 60	192
25	ttc ggc cac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag Phe Gly His Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys 65 70 75 80	240
30	cgg cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu 85 90 95	288
35	cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu 100 105 110	336
40	gtg aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly 115 120 125	384
45	atc gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr 130 135 140	432
50	aac tac aac agc cac aac gtc tat atc atg gcc gac aag cag aag aac Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn 145 150 155 160	480
55	ggc atc aag gtg aac ttc aag atc cgc cac aac atc gag gac ggc agc Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser 165 170 175	528
60	gtg cag ctc gcc gac cac tac cag cag aac acc ccc atc ggc gac Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp 180 185 190	573

BFP F1F, Y66H mutation, pos. 1 Met removed  
SEQ ID NOS:960 & 961

5	gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val 1 5 10 15	48
10	gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu 20 25 30	96
15	ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc tgc Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys 35 40 45	144
20	acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ttc Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe 50 55 60	192
25	ggc cac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag cgg Gly His Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg 65 70 75 80	240
30	cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg 85 90 95	288
35	acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag gtg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val 100 105 110	336
40	aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc atc Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile 115 120 125	384
45	gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn 130 135 140	432
50	tac aac agc cac aac gtc tat atc atg gcc gac aag cag aag aac ggc Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly 145 150 155 160	480
55	atc aag gtg aac ttc aag atc cgc cac aac atc gag gac ggc agc gtg Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val 165 170 175	528
60	cag ctc gcc gac cac tac cag cag aac acc ccc atc ggc gac Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp 180 185 190	570

BFP F1F, F64L,Y66H mutations  
SEQ ID NOS:962 & 963

55	atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu 1 5 10 15	48
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	gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc	96
	Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly	
	20 25 30	
5		
	gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc	144
	Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile	
	35 40 45	
10		
	tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc	192
	Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr	
	50 55 60	
15		
	ctg ggc cac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag	240
	Leu Gly His Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys	
	65 70 75 80	
20		
	cgg cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag	288
	Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu	
	85 90 95	
25		
	cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag	336
	Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu	
	100 105 110	
30		
	gtg aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc	384
	Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly	
	115 120 125	
35		
	atc gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac	432
	Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr	
	130 135 140	
40		
	aac tac aac agc cac aac gtc tat atc atg gcc gac aag cag aag aac	480
	Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn	
	145 150 155 160	
45		
	ggc atc aag gtg aac ttc aag atc cgc cac aac atc gag gac ggc agc	528
	Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser	
	165 170 175	
50		
	gtg cag ctc gcc gac cac tac cag cag aac acc ccc atc ggc gac	573
	Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp	
	180 185 190	
55		
	BFP F1F, F64L,Y66H mutations, pos. 1 Met removed	
	SEQ ID NOS:964 & 965	
50		
	gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc	48
	Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val	
	1 5 10 15	
55		
	gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag	96
	Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu	
	20 25 30	



	ggc	gag	ggc	gat	gcc	acc	tac	ggc	aag	ctg	acc	ctg	aag	ttc	atc	tgc	144
	Gly	Glu	Gly	Asp	Ala	Thr	Tyr	Gly	Lys	Leu	Thr	Leu	Lys	Phe	Ile	Cys	
			35					40					45				
5	acc	acc	ggc	aag	ctg	ccc	gtg	ccc	tgg	ccc	acc	ctc	gtg	acc	acc	ctg	192
	Thr	Thr	Gly	Lys	Leu	Pro	Val	Pro	Trp	Pro	Thr	Leu	Val	Thr	Thr	Leu	
			50				55					60					
10	ggc	cac	ggc	ctg	cag	tgc	ttc	gcc	cgc	tac	ccc	gac	cac	atg	aag	cgg	240
	Gly	His	Gly	Leu	Gln	Cys	Phe	Ala	Arg	Tyr	Pro	Asp	His	Met	Lys	Arg	
						70					75					80	
15	cac	gac	ttc	ttc	aag	tcc	gcc	atg	ccc	gaa	ggc	tac	gtc	cag	gag	cgc	288
	His	Asp	Phe	Phe	Lys	Ser	Ala	Met	Pro	Glu	Gly	Tyr	Val	Gln	Glu	Arg	
					85					90					95		
20	acc	atc	ttc	ttc	aag	gac	gac	ggc	aac	tac	aag	acc	cgc	gcc	gag	gtg	336
	Thr	Ile	Phe	Phe	Lys	Asp	Asp	Gly	Asn	Tyr	Lys	Thr	Arg	Ala	Glu	Val	
					100				105					110			
25	aag	ttc	gag	ggc	gac	acc	ctg	gtg	aac	cgc	atc	gag	ctg	aag	ggc	atc	384
	Lys	Phe	Glu	Gly	Asp	Thr	Leu	Val	Asn	Arg	Ile	Glu	Leu	Lys	Gly	Ile	
			115					120					125				
30	gac	ttc	aag	gag	gac	ggc	aac	atc	ctg	ggg	cac	aag	ctg	gag	tac	aac	432
	Asp	Phe	Lys	Glu	Asp	Gly	Asn	Ile	Leu	Gly	His	Lys	Leu	Glu	Tyr	Asn	
			130				135					140					
35	tac	aac	agc	cac	aac	gtc	tat	atc	atg	gcc	gac	aag	cag	aag	aac	ggc	480
	Tyr	Asn	Ser	His	Asn	Val	Tyr	Ile	Met	Ala	Asp	Lys	Gln	Lys	Asn	Gly	
						150					155					160	
40	atc	aag	gtg	aac	ttc	aag	atc	cgc	cac	aac	atc	gag	gac	ggc	agc	gtg	528
	Ile	Lys	Val	Asn	Phe	Lys	Ile	Arg	His	Asn	Ile	Glu	Asp	Gly	Ser	Val	
					165					170					175		
45	cag	ctc	gcc	gac	cac	tac	cag	cag	aac	acc	ccc	atc	ggc	gac			570
	Gln	Leu	Ala	Asp	His	Tyr	Gln	Gln	Asn	Thr	Pro	Ile	Gly	Asp			
				180					185					190			
	BFP F1F, F64L, Y66H, Y145F mutations																
	SEQ ID NOS:966 & 967																
50	atg	gtg	agc	aag	ggc	gag	gag	ctg	ttc	acc	ggg	gtg	gtg	ccc	atc	ctg	48
	Met	Val	Ser	Lys	Gly	Glu	Glu	Leu	Phe	Thr	Gly	Val	Val	Pro	Ile	Leu	
	1				5					10					15		
55	gtc	gag	ctg	gac	ggc	gac	gta	aac	ggc	cac	aag	ttc	agc	gtg	tcc	ggc	96
	Val	Glu	Leu	Asp	Gly	Asp	Val	Asn	Gly	His	Lys	Phe	Ser	Val	Ser	Gly	
				20					25					30			
60	gag	ggc	gag	ggc	gat	gcc	acc	tac	ggc	aag	ctg	acc	ctg	aag	ttc	atc	144
	Glu	Gly	Glu	Gly	Asp	Ala	Thr	Tyr	Gly	Lys	Leu	Thr	Leu	Lys	Phe	Ile	
			35					40					45				

	tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc	192														
	Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr															
	50 55 60															
5	ctg ggc cac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag	240														
	Leu Gly His Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys															
	65 70 75 80															
10	cgg cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag	288														
	Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu															
	85 90 95															
15	cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag	336														
	Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu															
	100 105 110															
20	gtg aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc	384														
	Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly															
	115 120 125															
25	atc gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac	432														
	Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr															
	130 135 140															
30	aac ttc aac agc cac aac gtc tat atc atg gcc gac aag cag aag aac	480														
	Asn Phe Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn															
	145 150 155 160															
35	ggc atc aag gtg aac ttc aag atc cgc cac aac atc gag gac ggc agc	528														
	Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser															
	165 170 175															
40	gtg cag ctc gcc gac cac tac cag cag aac acc ccc atc ggc gac	573														
	Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp															
	180 185 190															
45	BFP F1F, F64L, Y66H, Y145F mutations, pos. 1 Met removed															
	SEQ ID NOS:968 & 969															
50	gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc	48														
	Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val															
	1 5 10 15															
55	gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag	96														
	Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu															
	20 25 30															
60	ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc tgc	144														
	Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys															
	35 40 45															
65	acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ctg	192														
	Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Leu															
	50 55 60															

	ggc	cac	ggc	ctg	cag	tgc	ttc	gcc	cgc	tac	ccc	gac	cac	atg	aag	cgg	240
	Gly	His	Gly	Leu	Gln	Cys	Phe	Ala	Arg	Tyr	Pro	Asp	His	Met	Lys	Arg	
	65					70					75					80	
5	cac	gac	ttc	ttc	aag	tcc	gcc	atg	ccc	gaa	ggc	tac	gtc	cag	gag	cgc	288
	His	Asp	Phe	Phe	Lys	Ser	Ala	Met	Pro	Glu	Gly	Tyr	Val	Gln	Glu	Arg	
					85					90					95		
10	acc	atc	ttc	ttc	aag	gac	gac	ggc	aac	tac	aag	acc	cgc	gcc	gag	gtg	336
	Thr	Ile	Phe	Phe	Lys	Asp	Asp	Gly	Asn	Tyr	Lys	Thr	Arg	Ala	Glu	Val	
				100					105					110			
15	aag	ttc	gag	ggc	gac	acc	ctg	gtg	aac	cgc	atc	gag	ctg	aag	ggc	atc	384
	Lys	Phe	Glu	Gly	Asp	Thr	Leu	Val	Asn	Arg	Ile	Glu	Leu	Lys	Gly	Ile	
			115					120					125				
20	gac	ttc	aag	gag	gac	ggc	aac	atc	ctg	ggg	cac	aag	ctg	gag	tac	aac	432
	Asp	Phe	Lys	Glu	Asp	Gly	Asn	Ile	Leu	Gly	His	Lys	Leu	Glu	Tyr	Asn	
		130					135					140					
25	ttc	aac	agc	cac	aac	gtc	tat	atc	atg	gcc	gac	aag	cag	aag	aac	ggc	480
	Phe	Asn	Ser	His	Asn	Val	Tyr	Ile	Met	Ala	Asp	Lys	Gln	Lys	Asn	Gly	
	145					150					155					160	
30	atc	aag	gtg	aac	ttc	aag	atc	cgc	cac	aac	atc	gag	gac	ggc	agc	gtg	528
	Ile	Lys	Val	Asn	Phe	Lys	Ile	Arg	His	Asn	Ile	Glu	Asp	Gly	Ser	Val	
					165					170					175		
35	cag	ctc	gcc	gac	cac	tac	cag	cag	aac	acc	ccc	atc	ggc	gac			570
	Gln	Leu	Ala	Asp	His	Tyr	Gln	Gln	Asn	Thr	Pro	Ile	Gly	Asp			
				180					185					190			
40	BFP F1F, Y145F mutation SEQ ID NOS:970 & 971																
40	atg	gtg	agc	aag	ggc	gag	gag	ctg	ttc	acc	ggg	gtg	gtg	ccc	atc	ctg	48
	Met	Val	Ser	Lys	Gly	Glu	Glu	Leu	Phe	Thr	Gly	Val	Val	Pro	Ile	Leu	
	1				5					10					15		
45	gtc	gag	ctg	gac	ggc	gac	gta	aac	ggc	cac	aag	ttc	agc	gtg	tcc	ggc	96
	Val	Glu	Leu	Asp	Gly	Asp	Val	Asn	Gly	His	Lys	Phe	Ser	Val	Ser	Gly	
				20					25					30			
50	gag	ggc	gag	ggc	gat	gcc	acc	tac	ggc	aag	ctg	acc	ctg	aag	ttc	atc	144
	Glu	Gly	Glu	Gly	Asp	Ala	Thr	Tyr	Gly	Lys	Leu	Thr	Leu	Lys	Phe	Ile	
			35					40					45				
55	tgc	acc	acc	ggc	aag	ctg	ccc	gtg	ccc	tgg	ccc	acc	ctc	gtg	acc	acc	192
	Cys	Thr	Thr	Gly	Lys	Leu	Pro	Val	Pro	Trp	Pro	Thr	Leu	Val	Thr	Thr	
		50					55					60					
60	ttc	ggc	tac	ggc	ctg	cag	tgc	ttc	gcc	cgc	tac	ccc	gac	cac	atg	aag	240
	Phe	Gly	Tyr	Gly	Leu	Gln	Cys	Phe	Ala	Arg	Tyr	Pro	Asp	His	Met	Lys	
	65					70					75					80	

	cgg cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag	288
	Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu	
	85 90 95	
5	cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag	336
	Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu	
	100 105 110	
10	gtg aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc	384
	Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly	
	115 120 125	
15	atc gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac	432
	Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr	
	130 135 140	
20	aac ttc aac agc cac aac gtc tat atc atg gcc gac aag cag aag aac	480
	Asn Phe Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn	
	145 150 155 160	
	ggc atc aag gtg aac ttc aag atc cgc cac aac atc gag gac ggc agc	528
	Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser	
	165 170 175	
25	gtg cag ctc gcc gac cac tac cag cag aac acc ccc atc ggc gac	573
	Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp	
	180 185 190	
30	BFP F1F, Y145F mutation, pos. 1 Met removed	
	SEQ ID NOS:972 & 973	
35	gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc	48
	Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val	
	1 5 10 15	
40	gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag	96
	Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu	
	20 25 30	
45	ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc tgc	144
	Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys	
	35 40 45	
	acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ttc	192
	Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe	
	50 55 60	
50	ggc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag cgg	240
	Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg	
	65 70 75 80	
55	cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc	288
	His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg	
	85 90 95	

	acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag gtg	336
	Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val	
	100 105 110	
5	aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc atc	384
	Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile	
	115 120 125	
10	gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac	432
	Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn	
	130 135 140	
15	ttc aac agc cac aac gtc tat atc atg gcc gac aag cag aag aac ggc	480
	Phe Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly	
	145 150 155 160	
20	atc aag gtg aac ttc aag atc cgc cac aac atc gag gac ggc agc gtg	528
	Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val	
	165 170 175	
25	cag ctc gcc gac cac tac cag cag aac acc ccc atc ggc gac	570
	Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp	
	180 185 190	
30	atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg	48
	Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu	
	1 5 10 15	
35	gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc	96
	Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly	
	20 25 30	
40	gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ctg atc	144
	Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Leu Ile	
	35 40 45	
45	tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc	192
	Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr	
	50 55 60	
50	ctg ggc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag	240
	Leu Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys	
	65 70 75 80	
55	cgg cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag	288
	Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu	
	85 90 95	
55	cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag	336
	Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu	
	100 105 110	

Venus F1F, F46L, F64L, M153T, V163A mutations  
SEQ ID NOS:974 & 975

	gtg aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc	384
	Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly	
	115 120 125	
5	atc gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac	432
	Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr	
	130 135 140	
10	aac tac aac agc cac aac gtc tat atc acc gcc gac aag cag aag aac	480
	Asn Tyr Asn Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn	
	145 150 155 160	
15	ggc atc aag gtg aac ttc aag atc cgc cac aac atc gag gac ggc agc	528
	Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser	
	165 170 175	
20	gtg cag ctc gcc gac cac tac cag cag aac acc ccc atc ggc gac	573
	Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp	
	180 185 190	
Venus F1F, F46L, F64L, M153T, V163A mutations, pos. 1 Met removed		
SEQ ID NOS:976 & 977		
25	gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc	48
	Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val	
	1 5 10 15	
30	gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag	96
	Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu	
	20 25 30	
35	ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ctg atc tgc	144
	Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Leu Ile Cys	
	35 40 45	
40	acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ctg	192
	Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Leu	
	50 55 60	
45	ggc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag cgg	240
	Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg	
	65 70 75 80	
50	cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc	288
	His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg	
	85 90 95	
55	acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag gtg	336
	Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val	
	100 105 110	
55	aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc atc	384
	Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile	
	115 120 125	

	gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac	432
	Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn	
	130 135 140	
5	tac aac agc cac aac gtc tat atc acc gcc gac aag cag aag aac ggc	480
	Tyr Asn Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly	
	145 150 155 160	
10	atc aag gtg aac ttc aag atc cgc cac aac atc gag gac ggc agc gtg	528
	Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val	
	165 170 175	
15	cag ctc gcc gac cac tac cag cag aac acc ccc atc ggc gac	570
	Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp	
	180 185 190	
20	Venus FlF, V163A mutation	
	SEQ ID NOS:978 & 979	
25	atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg	48
	Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu	
	1 5 10 15	
30	gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc	96
	Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly	
	20 25 30	
35	gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc	144
	Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile	
	35 40 45	
40	tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc	192
	Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr	
	50 55 60	
45	ttc ggc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag	240
	Phe Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys	
	65 70 75 80	
50	cgg cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag	288
	Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu	
	85 90 95	
55	cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag	336
	Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu	
	100 105 110	
60	gtg aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc	384
	Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly	
	115 120 125	
65	atc gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac	432
	Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr	
	130 135 140	

	aac tac aac agc cac aac gtc tat atc atg gcc gac aag cag aag aac	480
	Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn	
	145 150 155 160	
5	ggc atc aag gcc aac ttc aag atc cgc cac aac atc gag gac ggc agc	528
	Gly Ile Lys Ala Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser	
	165 170 175	
10	gtg cag ctc gcc gac cac tac cag cag aac acc ccc atc ggc gac	573
	Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp	
	180 185 190	
15	Venus F1F, V163A mutation, pos. 1 Met removed	
	SEQ ID NOS:980 & 981	
	gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc	48
	Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val	
20	1 5 10 15	
	gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag	96
	Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu	
	20 25 30	
25	ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc tgc	144
	Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys	
	35 40 45	
30	acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ttc	192
	Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe	
	50 55 60	
	ggc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag cgg	240
	Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg	
35	65 70 75 80	
	cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc	288
	His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg	
40	85 90 95	
	acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag gtg	336
	Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val	
	100 105 110	
45	aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc atc	384
	Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile	
	115 120 125	
50	gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac	432
	Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn	
	130 135 140	
	tac aac agc cac aac gtc tat atc atg gcc gac aag cag aag aac ggc	480
	Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly	
55	145 150 155 160	



	atc aag gcc aac ttc aag atc cgc cac aac atc gag gac ggc agc gtg	528
	Ile Lys Ala Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val	
	165 170 175	
5	cag ctc gcc gac cac tac cag cag aac acc ccc atc ggc gac	570
	Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp	
	180 185 190	
10	Venus F1F, M153T,V163A mutations SEQ ID NOS:982 & 983	
15	atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg	48
	Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu	
	1 5 10 15	
20	gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc	96
	Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly	
	20 25 30	
25	gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc	144
	Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile	
	35 40 45	
30	tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc	192
	Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr	
	50 55 60	
35	ttc ggc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag	240
	Phe Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys	
	65 70 75 80	
40	cgg cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag	288
	Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu	
	85 90 95	
45	cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag	336
	Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu	
	100 105 110	
50	gtg aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc	384
	Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly	
	115 120 125	
55	atc gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac	432
	Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr	
	130 135 140	
60	aac tac aac agc cac aac gtc tat atc acc gcc gac aag cag aag aac	480
	Asn Tyr Asn Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn	
	145 150 155 160	
65	ggc atc aag gcc aac ttc aag atc cgc cac aac atc gag gac ggc agc	528
	Gly Ile Lys Ala Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser	
	165 170 175	

	gtg cag ctc gcc gac cac tac cag cag aac acc ccc atc ggc gac	573
	Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp	
	180 185 190	
5	Venus F1F, M153T,V163A mutations, pos. 1 Met removed SEQ ID NOS:984 & 985	
10	gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc	48
	Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val	
	1 5 10 15	
15	gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag	96
	Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu	
	20 25 30	
20	ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc tgc	144
	Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys	
	35 40 45	
25	acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ttc	192
	Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe	
	50 55 60	
30	ggc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag cgg	240
	Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg	
	65 70 75 80	
35	cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc	288
	His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg	
	85 90 95	
40	acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag gtg	336
	Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val	
	100 105 110	
45	aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc atc	384
	Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile	
	115 120 125	
50	gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac	432
	Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn	
	130 135 140	
55	tac aac agc cac aac gtc tat atc acc gcc gac aag cag aag aac ggc	480
	Tyr Asn Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly	
	145 150 155 160	
60	atc aag gcc aac ttc aag atc cgc cac aac atc gag gac ggc agc gtg	528
	Ile Lys Ala Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val	
	165 170 175	
65	cag ctc gcc gac cac tac cag cag aac acc ccc atc ggc gac	570
	Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp	
	180 185 190	

Venus FlF, S175G mutation  
SEQ ID NOS:986 & 987

5	atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu 1 5 10 15	48
10	gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly 20 25 30	96
15	gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile 35 40 45	144
20	tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr 50 55 60	192
25	ttc ggc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag Phe Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys 65 70 75 80	240
30	cgg cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu 85 90 95	288
35	cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu 100 105 110	336
40	gtg aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly 115 120 125	384
45	atc gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr 130 135 140	432
50	aac tac aac agc cac aac gtc tat atc atg gcc gac aag cag aag aac Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn 145 150 155 160	480
55	ggc atc aag gtg aac ttc aag atc cgc cac aac atc gag gac ggc ggc Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Gly 165 170 175	528
60	gtg cag ctc gcc gac cac tac cag cag aac acc ccc atc ggc gac Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp 180 185 190	573

Venus FlF, S175G mutation, pos. 1 Met removed  
SEQ ID NOS:988 & 989

55	gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val 1 5 10 15	48
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	gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag	96
	Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu	
	20 25 30	
5	ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc tgc	144
	Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys	
	35 40 45	
10	acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ttc	192
	Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe	
	50 55 60	
15	ggc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag cgg	240
	Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg	
	65 70 75 80	
20	cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc	288
	His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg	
	85 90 95	
25	acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag gtg	336
	Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val	
	100 105 110	
30	aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc atc	384
	Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile	
	115 120 125	
35	gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac	432
	Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn	
	130 135 140	
40	tac aac agc cac aac gtc tat atc atg gcc gac aag cag aag aac ggc	480
	Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly	
	145 150 155 160	
45	atc aag gtg aac ttc aag atc cgc cac aac atc gag gac ggc ggc gtg	528
	Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Gly Val	
	165 170 175	
50	cag ctc gcc gac cac tac cag cag aac acc ccc atc ggc gac	570
	Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp	
	180 185 190	
Venus F1F, M153T,S175G mutations		
SEQ ID NOS:990 & 991		
55	atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg	48
	Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu	
	1 5 10 15	
55	gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc	96
	Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly	
	20 25 30	

	gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc	144
	Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile	
	35 40 45	
5	tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc	192
	Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr	
	50 55 60	
10	ttc ggc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag	240
	Phe Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys	
	65 70 75 80	
15	cgg cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag	288
	Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu	
	85 90 95	
20	cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag	336
	Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu	
	100 105 110	
25	gtg aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc	384
	Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly	
	115 120 125	
30	atc gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac	432
	Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr	
	130 135 140	
35	aac tac aac agc cac aac gtc tat atc acc gcc gac aag cag aag aac	480
	Asn Tyr Asn Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn	
	145 150 155 160	
40	ggc atc aag gtg aac ttc aag atc cgc cac aac atc gag gac ggc ggc	528
	Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Gly	
	165 170 175	
45	gtg cag ctc gcc gac cac tac cag cag aac acc ccc atc ggc gac	573
	Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp	
	180 185 190	
Venus F1F, M153T,S175G mutations, pos. 1 Met removed		
SEQ ID NOS:992 & 993		
50	gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc	48
	Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val	
	1 5 10 15	
55	gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag	96
	Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu	
	20 25 30	
60	ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc tgc	144
	Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys	
	35 40 45	

	acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ttc	192
	Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe	
	50 55 60	
5	ggc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag cgg	240
	Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg	
	65 70 75 80	
10	cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc	288
	His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg	
	85 90 95	
15	acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag gtg	336
	Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val	
	100 105 110	
20	aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc atc	384
	Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile	
	115 120 125	
25	gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac	432
	Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn	
	130 135 140	
30	tac aac agc cac aac gtc tat atc acc gcc gac aag cag aag aac ggc	480
	Tyr Asn Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly	
	145 150 155 160	
35	atc aag gtg aac ttc aag atc cgc cac aac atc gag gac ggc ggc gtg	528
	Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Gly Val	
	165 170 175	
40	cag ctc gcc gac cac tac cag cag aac acc ccc atc ggc gac	570
	Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp	
	180 185 190	
Venus F1F, V163A, S175G mutations		
40	SEQ ID NOS:994 & 995	
45	atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg	48
	Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu	
	1 5 10 15	
50	gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc	96
	Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly	
	20 25 30	
55	gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc	144
	Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile	
	35 40 45	
60	tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc	192
	Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr	
	50 55 60	

	ttc ggc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag	240
	Phe Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys	
	65 70 75 80	
5	cgg cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag	288
	Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu	
	85 90 95	
10	cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag	336
	Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu	
	100 105 110	
15	gtg aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc	384
	Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly	
	115 120 125	
20	atc gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac	432
	Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr	
	130 135 140	
25	aac tac aac agc cac aac gtc tat atc atg gcc gac aag cag aag aac	480
	Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn	
	145 150 155 160	
30	ggc atc aag gcc aac ttc aag atc cgc cac aac atc gag gac ggc ggc	528
	Gly Ile Lys Ala Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Gly	
	165 170 175	
35	gtg cag ctg gcc gac cac tac cag cag aac acc ccc atc ggc gac	573
	Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp	
	180 185 190	
35	Venus F1F, V163A, S175G mutations, pos. 1 Met removed	
	SEQ ID NOS: 996 & 997	
40	gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc	48
	Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val	
	1 5 10 15	
45	gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag	96
	Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu	
	20 25 30	
50	ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc tgc	144
	Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys	
	35 40 45	
55	acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ttc	192
	Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe	
	50 55 60	
55	ggc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag cgg	240
	Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg	
	65 70 75 80	

	cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc	288
	His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg	
	85 90 95	
5	acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag gtg	336
	Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val	
	100 105 110	
10	aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc atc	384
	Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile	
	115 120 125	
15	gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac	432
	Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn	
	130 135 140	
20	tac aac agc cac aac gtc tat atc atg gcc gac aag cag aag aac ggc	480
	Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly	
	145 150 155 160	
	atc aag gcc aac ttc aag atc cgc cac aac atc gag gac ggc ggc gtg	528
	Ile Lys Ala Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Gly Val	
	165 170 175	
25	cag ctc gcc gac cac tac cag cag aac acc ccc atc ggc gac	570
	Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp	
	180 185 190	
30	Venus F1F, M153T, V163A, S175G mutations SEQ ID NOS:998 & 999	
35	atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg	48
	Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu	
	1 5 10 15	
40	gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc	96
	Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly	
	20 25 30	
45	gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc	144
	Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile	
	35 40 45	
	tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc	192
	Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr	
	50 55 60	
50	ttc ggc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag	240
	Phe Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys	
	65 70 75 80	
55	cgg cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag	288
	Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu	
	85 90 95	



	cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag	336														
	Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu															
	100 105 110															
5	gtg aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc	384														
	Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly															
	115 120 125															
10	atc gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac	432														
	Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr															
	130 135 140															
15	aac tac aac agc cac aac gtc tat atc acc gcc gac aag cag aag aac	480														
	Asn Tyr Asn Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn															
	145 150 155 160															
20	ggc atc aag gcc aac ttc aag atc cgc cac aac atc gag gac ggc ggc	528														
	Gly Ile Lys Ala Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Gly															
	165 170 175															
	gtg cag ctc gcc gac cac tac cag cag aac acc ccc atc ggc gac	573														
	Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp															
	180 185 190															
25	Venus F1F, M153T,V163A, S175G mutations,pos. 1 Met removed SEQ ID NOS:1000 & 1001															
30	gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc	48														
	Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val															
	1 5 10 15															
35	gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag	96														
	Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu															
	20 25 30															
40	ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc tgc	144														
	Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys															
	35 40 45															
45	acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ttc	192														
	Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe															
	50 55 60															
	ggc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag cgg	240														
	Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg															
	65 70 75 80															
50	cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc	288														
	His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg															
	85 90 95															
55	acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag gtg	336														
	Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val															
	100 105 110															

	aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc atc	384
	Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile	
	115 120 125	
5	gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac	432
	Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn	
	130 135 140	
10	tac aac agc cac aac gtc tat atc acc gcc gag aag cag aag aac ggc	480
	Tyr Asn Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly	
	145 150 155 160	
15	atc aag gcc aac ttc aag atc cgc cac aac atc gag gac ggc ggc gtg	528
	Ile Lys Ala Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Gly Val	
	165 170 175	
20	cag ctc gcc gac cac tac cag cag aac acc ccc atc ggc gac	570
	Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp	
	180 185 190	
Venus F1F, F46L, F64L, M153T, V163A, S175G mutations		
SEQ ID NOS:1002 & 1003		
25	atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg	48
	Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu	
	1 5 10 15	
30	gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc	96
	Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly	
	20 25 30	
35	gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ctg atc	144
	Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Leu Ile	
	35 40 45	
40	tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc	192
	Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr	
	50 55 60	
45	ctg ggc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag	240
	Leu Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys	
	65 70 75 80	
50	cgg cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag	288
	Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu	
	85 90 95	
55	cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag	336
	Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu	
	100 105 110	
55	gtg aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc	384
	Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly	
	115 120 125	

	atc gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac	432
	Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr	
	130 135 140	
5	aac tac aac agc cac aac gtc tat atc acc gcc gac aag cag aag aac	480
	Asn Tyr Asn Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn	
	145 150 155 160	
10	ggc atc aag gcc aac ttc aag atc cgc cac aac atc gag gac ggc ggc	528
	Gly Ile Lys Ala Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Gly	
	165 170 175	
15	gtg cag ctc gcc gac cac tac cag cag aac acc ccc atc ggc gac	573
	Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp	
	180 185 190	
20	Venus F1F, F46L, F64L, M153T, V163A, S175G mutations, pos. 1 Met removed SEQ ID NOS:1004 & 1005	
25	gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc	48
	Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val	
	1 5 10 15	
30	gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag	96
	Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu	
	20 25 30	
35	ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ctg atc tgc	144
	Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Leu Ile Cys	
	35 40 45	
40	acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ctg	192
	Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Leu	
	50 55 60	
45	ggc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag cgg	240
	Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg	
	65 70 75 80	
50	cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc	288
	His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg	
	85 90 95	
55	acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag gtg	336
	Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val	
	100 105 110	
60	aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc atc	384
	Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile	
	115 120 125	
65	gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac	432
	Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn	
	130 135 140	

	tac aac agc cac aac gtc tat atc acc gcc gac aag cag aag aac ggc	480
	Tyr Asn Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly	
	145 150 155 160	
5	atc aag gcc aac ttc aag atc cgc cac aac atc gag gac ggc ggc gtg	528
	Ile Lys Ala Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Gly Val	
	165 170 175	
10	cag ctc gcc gac cac tac cag cag aac acc ccc atc ggc gac	570
	Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp	
	180 185 190	
15	YFP F2F, Met added @ pos. 1 (YFP F2F corresponds to aa residues 192-end of YFP) SEQ ID NOS:1006 & 1007	
20	atg ggc ccc gtg ctg ctg ccc gac aac cac tac ctg agc tac cag tcc	48
	Met Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Tyr Gln Ser	
	1 5 10 15	
25	gcc ctg agc aaa gac ccc aac gag aag cgc gat cac atg gtc ctg ctg	96
	Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu	
	20 25 30	
30	gag ttc gtg acc gcc gcc ggg atc act ctc ggc atg gac gag ctg tac	144
	Glu Phe Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr	
	35 40 45	
35	aag	147
	Lys	
40	YFP F2F, Y203F mutation SEQ ID NOS:1008 & 1009	
40	ggc ccc gtg ctg ctg ccc gac aac cac tac ctg agc ttc cag tcc gcc	48
	Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Phe Gln Ser Ala	
	1 5 10 15	
45	ctg agc aaa gac ccc aac gag aag cgc gat cac atg gtc ctg ctg gag	96
	Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu	
	20 25 30	
50	ttc gtg acc gcc gcc ggg atc act ctc ggc atg gac gag ctg tac aag	144
	Phe Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys	
	35 40 45	
55	YFP F2F, Y203F mutation, Met added @ pos.1 SEQ ID NOS:1010 & 1011	
55	atg ggc ccc gtg ctg ctg ccc gac aac cac tac ctg agc ttc cag tcc	48
	Met Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Phe Gln Ser	
	1 5 10 15	

	gcc ctg agc aaa gac ccc aac gag aag cgc gat cac atg gtc ctg ctg	96
	Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu	
	20 25 30	
5	gag ttc gtg acc gcc gcc ggg atc act ctc ggc atg gac gag ctg tac	144
	Glu Phe Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr	
	35 40 45	
10	aag	147
	Lys	
15	YFP F2F, Y203H mutation	
	SEQ ID NOS:1012 & 1013	
	ggc ccc gtg ctg ctg ccc gac aac cac tac ctg agc cac cag tcc gcc	48
	Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser His Gln Ser Ala	
	1 5 10 15	
20	ctg agc aaa gac ccc aac gag aag cgc gat cac atg gtc ctg ctg gag	96
	Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu	
	20 25 30	
25	ttc gtg acc gcc gcc ggg atc act ctc ggc atg gac gag ctg tac aag	144
	Phe Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys	
	35 40 45	
30	YFP F2F, Y203H mutation, Met added @ pos. 1	
	SEQ ID NOS:1014 & 1015	
	atg ggc ccc gtg ctg ctg ccc gac aac cac tac ctg agc cac cag tcc	48
	Met Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser His Gln Ser	
	1 5 10 15	
35	gcc ctg agc aaa gac ccc aac gag aag cgc gat cac atg gtc ctg ctg	96
	Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu	
	20 25 30	
40	gag ttc gtg acc gcc gcc ggg atc act ctc ggc atg gac gag ctg tac	144
	Glu Phe Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr	
	35 40 45	
45	aag	147
	Lys	
50	YFP F2F, Y203T mutation	
	SEQ ID NOS:1016 & 1017	
	ggc ccc gtg ctg ctg ccc gac aac cac tac ctg agc acc cag tcc gcc	48
	Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala	
	1 5 10 15	
55	ctg agc aaa gac ccc aac gag aag cgc gat cac atg gtc ctg ctg gag	96
	Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu	
	20 25 30	

ttc gtg acc gcc gcc ggg atc act ctc ggc atg gac gag ctg tac aag 144  
 Phe Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys  
 35 40 45  
 5  
 YFP F2F, Y203T mutation, Met added @ pos. 1  
 SEQ ID NOS:1018 & 1019  
 10 atg ggc ccc gtg ctg ctg ccc gac aac cac tac ctg agc acc cag tcc 48  
 Met Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser  
 1 5 10 15  
 15 gcc ctg agc aaa gac ccc aac gag aag cgc gat cac atg gtc ctg ctg 96  
 Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu  
 20 25 30  
 20 gag ttc gtg acc gcc gcc ggg atc act ctc ggc atg gac gag ctg tac 144  
 Glu Phe Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr  
 35 40 45  
 aag 147  
 Lys  
 25  
 RFP F1A, pos. 1 Met removed  
 (RFP F1A corresponds to aa residues 1-39 of mRFP)  
 SEQ ID NOS:1020 & 1021  
 30 gcc tcc tcc gag gac gtc atc aag gag ttc atg cgc ttc aag gtg cgc 48  
 Ala Ser Ser Glu Asp Val Ile Lys Glu Phe Met Arg Phe Lys Val Arg  
 1 5 10 15  
 35 atg gag ggc tcc gtg aac ggc cac gag ttc gag atc gag ggc gag ggc 96  
 Met Glu Gly Ser Val Asn Gly His Glu Phe Glu Ile Glu Gly Glu Gly  
 20 25 30  
 gag ggc cgc ccc tac gag 114  
 Glu Gly Arg Pro Tyr Glu  
 40 35  
 RFP F2A, Met added @ pos. 1  
 (RFP F2A corresponds to aa residues 40-end of mRFP)  
 45 SEQ ID NOS:1022 & 1023  
 atg ggc acc cag acc gcc aag ctg aag gtg acc aag ggc ggc ccc ctg 48  
 Met Gly Thr Gln Thr Ala Lys Leu Lys Val Thr Lys Gly Gly Pro Leu  
 1 5 10 15  
 50 ccc ttc gcc tgg gac atc ctg tcc cct cag ttc cag tac ggc tcc aag 96  
 Pro Phe Ala Trp Asp Ile Leu Ser Pro Gln Phe Gln Tyr Gly Ser Lys  
 20 25 30  
 55 gcc tac gtg aag cac ccc gcc gac atc ccc gac tac ttg aag ctg tcc 144  
 Ala Tyr Val Lys His Pro Ala Asp Ile Pro Asp Tyr Leu Lys Leu Ser  
 35 40 45

	ttc ccc gag ggc ttc aag tgg gag cgc gtg atg aac ttc gag gac ggc	192
	Phe Pro Glu Gly Phe Lys Trp Glu Arg Val Met Asn Phe Glu Asp Gly	
	50 55 60	
5	ggc gtg gtg acc gtg acc cag gac tcc tcc ctg cag gac ggc gag ttc	240
	Gly Val Val Thr Val Thr Gln Asp Ser Ser Leu Gln Asp Gly Glu Phe	
	65 70 75 80	
10	atc tac aag gtg aag ctg cgc ggc acc aac ttc ccc tcc gac ggc ccc	288
	Ile Tyr Lys Val Lys Leu Arg Gly Thr Asn Phe Pro Ser Asp Gly Pro	
	85 90 95	
15	gta atg cag aag aag acc atg ggc tgg gag gcc tcc acc gag cgg atg	336
	Val Met Gln Lys Lys Thr Met Gly Trp Glu Ala Ser Thr Glu Arg Met	
	100 105 110	
20	tac ccc gag gac ggc gcc ctg aag ggc gag atc aag atg agg ctg aag	384
	Tyr Pro Glu Asp Gly Ala Leu Lys Gly Glu Ile Lys Met Arg Leu Lys	
	115 120 125	
25	ctg aag gac ggc ggc cac tac gac gcc gag gtc aag acc acc tac atg	432
	Leu Lys Asp Gly Gly His Tyr Asp Ala Glu Val Lys Thr Thr Tyr Met	
	130 135 140	
30	gcc aag aag ccc gtg cag ctg ccc ggc gcc tac aag acc gac atc aag	480
	Ala Lys Lys Pro Val Gln Leu Pro Gly Ala Tyr Lys Thr Asp Ile Lys	
	145 150 155 160	
35	ctg gac atc acc tcc cac aac gag gac tac acc atc gtg gaa cag tac	528
	Leu Asp Ile Thr Ser His Asn Glu Asp Tyr Thr Ile Val Glu Gln Tyr	
	165 170 175	
40	gag cgc gcc gag ggc cgc cac tcc acc ggc gcc	561
	Glu Arg Ala Glu Gly Arg His Ser Thr Gly Ala	
	180 185	
40	RFP F1B, pos. 1 Met removed (RFP F1B corresponds to aa residues 1-100 of mRFP) SEQ ID NOS:1024 & 1025	
45	gcc tcc tcc gag gac gtc atc aag gag ttc atg cgc ttc aag gtg cgc	48
	Ala Ser Ser Glu Asp Val Ile Lys Glu Phe Met Arg Phe Lys Val Arg	
	1 5 10 15	
50	atg gag ggc tcc gtg aac ggc cac gag ttc gag atc gag ggc gag ggc	96
	Met Glu Gly Ser Val Asn Gly His Glu Phe Glu Ile Glu Gly Glu Gly	
	20 25 30	
55	gag ggc cgc ccc tac gag ggc acc cag acc gcc aag ctg aag gtg acc	144
	Glu Gly Arg Pro Tyr Glu Gly Thr Gln Thr Ala Lys Leu Lys Val Thr	
	35 40 45	
55	aag ggc ggc ccc ctg ccc ttc gcc tgg gac atc ctg tcc cct cag ttc	192
	Lys Gly Gly Pro Leu Pro Phe Ala Trp Asp Ile Leu Ser Pro Gln Phe	
	50 55 60	

	cag	tac	ggc	tcc	aag	gcc	tac	gtg	aag	cac	ccc	gcc	gac	atc	ccc	gac	240
	Gln	Tyr	Gly	Ser	Lys	Ala	Tyr	Val	Lys	His	Pro	Ala	Asp	Ile	Pro	Asp	
	65					70					75					80	
5	tac	ttg	aag	ctg	tcc	ttc	ccc	gag	ggc	ttc	aag	tgg	gag	cgc	gtg	atg	288
	Tyr	Leu	Lys	Leu	Ser	Phe	Pro	Glu	Gly	Phe	Lys	Trp	Glu	Arg	Val	Met	
					85					90					95		
10	aac	ttc	gag	gac													300
	Asn	Phe	Glu	Asp													
					100												
	RFP F2B, Met added @ pos. 1																
15	(RFP F2B corresponds to aa residues 102-225(end) of mRFP)																
	SEQ ID NOS:1026 & 1027																
	atg	ggc	ggc	gtg	gtg	acc	gtg	acc	cag	gac	tcc	tcc	ctg	cag	gac	ggc	48
	Met	Gly	Gly	Val	Val	Thr	Val	Thr	Gln	Asp	Ser	Ser	Leu	Gln	Asp	Gly	
20	1				5					10					15		
	gag	ttc	atc	tac	aag	gtg	aag	ctg	cgc	ggc	acc	aac	ttc	ccc	tcc	gac	96
	Glu	Phe	Ile	Tyr	Lys	Val	Lys	Leu	Arg	Gly	Thr	Asn	Phe	Pro	Ser	Asp	
				20					25					30			
25	ggc	ccc	gta	atg	cag	aag	aag	acc	atg	ggc	tgg	gag	gcc	tcc	acc	gag	144
	Gly	Pro	Val	Met	Gln	Lys	Lys	Thr	Met	Gly	Trp	Glu	Ala	Ser	Thr	Glu	
				35				40					45				
30	cgg	atg	tac	ccc	gag	gac	ggc	gcc	ctg	aag	ggc	gag	atc	aag	atg	agg	192
	Arg	Met	Tyr	Pro	Glu	Asp	Gly	Ala	Leu	Lys	Gly	Glu	Ile	Lys	Met	Arg	
		50					55					60					
	ctg	aag	ctg	aag	gac	ggc	ggc	cac	tac	gac	gcc	gag	gtc	aag	acc	acc	240
35	Leu	Lys	Leu	Lys	Asp	Gly	Gly	His	Tyr	Asp	Ala	Glu	Val	Lys	Thr	Thr	
	65					70					75					80	
	tac	atg	gcc	aag	aag	ccc	gtg	cag	ctg	ccc	ggc	gcc	tac	aag	acc	gac	288
40	Tyr	Met	Ala	Lys	Lys	Pro	Val	Gln	Leu	Pro	Gly	Ala	Tyr	Lys	Thr	Asp	
					85					90					95		
	atc	aag	ctg	gac	atc	acc	tcc	cac	aac	gag	gac	tac	acc	atc	gtg	gaa	336
	Ile	Lys	Leu	Asp	Ile	Thr	Ser	His	Asn	Glu	Asp	Tyr	Thr	Ile	Val	Glu	
				100					105					110			
45	cag	tac	gag	cgc	gcc	gag	ggc	cgc	cac	tcc	acc	ggc	gcc				375
	Gln	Tyr	Glu	Arg	Ala	Glu	Gly	Arg	His	Ser	Thr	Gly	Ala				
				115				120					125				
50	RFP F1C, pos. 1 Met removed																



	atg gag ggc tcc gtg aac ggc cac gag ttc gag atc gag ggc gag ggc	96
	Met Glu Gly Ser Val Asn Gly His Glu Phe Glu Ile Glu Gly Glu Gly	
	20 25 30	
5		
	gag ggc cgc ccc tac gag ggc acc cag acc gcc aag ctg aag gtg acc	144
	Glu Gly Arg Pro Tyr Glu Gly Thr Gln Thr Ala Lys Leu Lys Val Thr	
	35 40 45	
10		
	aag ggc ggc ccc ctg ccc ttc gcc tgg gac atc ctg tcc cct cag ttc	192
	Lys Gly Gly Pro Leu Pro Phe Ala Trp Asp Ile Leu Ser Pro Gln Phe	
	50 55 60	
15		
	cag tac ggc tcc aag gcc tac gtg aag cac ccc gcc gac atc ccc gac	240
	Gln Tyr Gly Ser Lys Ala Tyr Val Lys His Pro Ala Asp Ile Pro Asp	
	65 70 75 80	
20		
	tac ttg aag ctg tcc ttc ccc gag ggc ttc aag tgg gag cgc gtg atg	288
	Tyr Leu Lys Leu Ser Phe Pro Glu Gly Phe Lys Trp Glu Arg Val Met	
	85 90 95	
25		
	aac ttc gag gac ggc ggc gtg gtg acc gtg acc cag gac tcc tcc ctg	336
	Asn Phe Glu Asp Gly Gly Val Val Thr Val Thr Gln Asp Ser Ser Leu	
	100 105 110	
30		
	cag gac	342
	Gln Asp	
35		
	RFP F2C, Met added @ pos. 1	
	(RFP F2C corresponds to aa residues 116-225(end) of mRFP)	
	SEQ ID NOS:1030 & 1031	
40		
	atg ggc gag ttc atc tac aag gtg aag ctg cgc ggc acc aac ttc ccc	48
	Met Gly Glu Phe Ile Tyr Lys Val Lys Leu Arg Gly Thr Asn Phe Pro	
	1 5 10 15	
45		
	tcc gac ggc ccc gta atg cag aag aag acc atg ggc tgg gag gcc tcc	96
	Ser Asp Gly Pro Val Met Gln Lys Lys Thr Met Gly Trp Glu Ala Ser	
	20 25 30	
50		
	acc gag cgg atg tac ccc gag gac ggc gcc ctg aag ggc gag atc aag	144
	Thr Glu Arg Met Tyr Pro Glu Asp Gly Ala Leu Lys Gly Glu Ile Lys	
	35 40 45	
55		
	atg agg ctg aag ctg aag gac ggc ggc cac tac gac gcc gag gtc aag	192
	Met Arg Leu Lys Leu Lys Asp Gly Gly His Tyr Asp Ala Glu Val Lys	
	50 55 60	
60		
	acc acc tac atg gcc aag aag ccc gtg cag ctg ccc ggc gcc tac aag	240
	Thr Thr Tyr Met Ala Lys Lys Pro Val Gln Leu Pro Gly Ala Tyr Lys	
	65 70 75 80	
65		
	acc gac atc aag ctg gac atc acc tcc cac aac gag gac tac acc atc	288
	Thr Asp Ile Lys Leu Asp Ile Thr Ser His Asn Glu Asp Tyr Thr Ile	
	85 90 95	

	gtg gaa cag tac gag cgc gcc gag ggc cgc cac tcc acc ggc gcc	333
	Val Glu Gln Tyr Glu Arg Ala Glu Gly Arg His Ser Thr Gly Ala	
	100 105 110	
5		
	RFP F1D, pos. 1 Met removed (RFP F1D corresponds to aa residues 1-153 of mRFP) SEQ ID NOS:1032 & 1033	
10		
	gcc tcc tcc gag gac gtc atc aag gag ttc atg cgc ttc aag gtg cgc	48
	Ala Ser Ser Glu Asp Val Ile Lys Glu Phe Met Arg Phe Lys Val Arg	
	1 5 10 15	
15		
	atg gag ggc tcc gtg aac ggc cac gag ttc gag atc gag ggc gag ggc	96
	Met Glu Gly Ser Val Asn Gly His Glu Phe Glu Ile Glu Gly Glu Gly	
	20 25 30	
20		
	gag ggc cgc ccc tac gag ggc acc cag acc gcc aag ctg aag gtg acc	144
	Glu Gly Arg Pro Tyr Glu Gly Thr Gln Thr Ala Lys Leu Lys Val Thr	
	35 40 45	
25		
	aag ggc ggc ccc ctg ccc ttc gcc tgg gac atc ctg tcc cct cag ttc	192
	Lys Gly Gly Pro Leu Pro Phe Ala Trp Asp Ile Leu Ser Pro Gln Phe	
	50 55 60	
30		
	cag tac ggc tcc aag gcc tac gtg aag cac ccc gcc gac atc ccc gac	240
	Gln Tyr Gly Ser Lys Ala Tyr Val Lys His Pro Ala Asp Ile Pro Asp	
	65 70 75 80	
35		
	tac ttg aag ctg tcc ttc ccc gag ggc ttc aag tgg gag cgc gtg atg	288
	Tyr Leu Lys Leu Ser Phe Pro Glu Gly Phe Lys Trp Glu Arg Val Met	
	85 90 95	
40		
	aac ttc gag gac ggc ggc gtg gtg acc gtg acc cag gac tcc tcc ctg	336
	Asn Phe Glu Asp Gly Gly Val Val Thr Val Thr Gln Asp Ser Ser Leu	
	100 105 110	
45		
	cag gac ggc gag ttc atc tac aag gtg aag ctg cgc ggc acc aac ttc	384
	Gln Asp Gly Glu Phe Ile Tyr Lys Val Lys Leu Arg Gly Thr Asn Phe	
	115 120 125	
50		
	ccc tcc gac ggc ccc gta atg cag aag aag acc atg ggc tgg gag gcc	432
	Pro Ser Asp Gly Pro Val Met Gln Lys Lys Thr Met Gly Trp Glu Ala	
	130 135 140	
55		
	tcc acc gag cgg atg tac ccc gag	456
	Ser Thr Glu Arg Met Tyr Pro Glu	
	145 150	
	RFP F2D, Met added @ pos. 1 (RFP F2D corresponds to aa residues 154-225(end) of mRFP) SEQ ID NOS:1034 & 1035	
55		
	atg gac ggc gcc ctg aag ggc gag atc aag atg agg ctg aag ctg aag	48
	Met Asp Gly Ala Leu Lys Gly Glu Ile Lys Met Arg Leu Lys Leu Lys	
	1 5 10 15	

	gac ggc ggc cac tac gac gcc gag gtc aag acc acc tac atg gcc aag	96
	Asp Gly Gly His Tyr Asp Ala Glu Val Lys Thr Thr Tyr Met Ala Lys	
	20 25 30	
5	aag ccc gtg cag ctg ccc ggc gcc tac aag acc gac atc aag ctg gac	144
	Lys Pro Val Gln Leu Pro Gly Ala Tyr Lys Thr Asp Ile Lys Leu Asp	
	35 40 45	
10	atc acc tcc cac aac gag gac tac acc atc gtg gaa cag tac gag cgc	192
	Ile Thr Ser His Asn Glu Asp Tyr Thr Ile Val Glu Gln Tyr Glu Arg	
	50 55 60	
15	gcc gag ggc cgc cac tcc acc ggc gcc	219
	Ala Glu Gly Arg His Ser Thr Gly Ala	
	65 70	
20	RFP F1E, pos. 1 Met removed (RFP F1E corresponds to aa residues 1-169 of mRFP) SEQ ID NOS:1036 & 1037	
25	gcc tcc tcc gag gac gtc atc aag gag ttc atg cgc ttc aag gtg cgc	48
	Ala Ser Ser Glu Asp Val Ile Lys Glu Phe Met Arg Phe Lys Val Arg	
	1 5 10 15	
30	atg gag ggc tcc gtg aac ggc cac gag ttc gag atc gag ggc gag ggc	96
	Met Glu Gly Ser Val Asn Gly His Glu Phe Glu Ile Glu Gly Glu Gly	
	20 25 30	
35	gag ggc cgc ccc tac gag ggc acc cag acc gcc aag ctg aag gtg acc	144
	Glu Gly Arg Pro Tyr Glu Gly Thr Gln Thr Ala Lys Leu Lys Val Thr	
	35 40 45	
40	aag ggc ggc ccc ctg ccc ttc gcc tgg gac atc ctg tcc cct cag ttc	192
	Lys Gly Gly Pro Leu Pro Phe Ala Trp Asp Ile Leu Ser Pro Gln Phe	
	50 55 60	
45	cag tac ggc tcc aag gcc tac gtg aag cac ccc gcc gac atc ccc gac	240
	Gln Tyr Gly Ser Lys Ala Tyr Val Lys His Pro Ala Asp Ile Pro Asp	
	65 70 75 80	
50	tac ttg aag ctg tcc ttc ccc gag ggc ttc aag tgg gag cgc gtg atg	288
	Tyr Leu Lys Leu Ser Phe Pro Glu Gly Phe Lys Trp Glu Arg Val Met	
	85 90 95	
55	aac ttc gag gac ggc ggc gtg gtg acc gtg acc cag gac tcc tcc ctg	336
	Asn Phe Glu Asp Gly Gly Val Val Thr Val Thr Gln Asp Ser Ser Leu	
	100 105 110	
60	cag gac ggc gag ttc atc tac aag gtg aag ctg cgc ggc acc aac ttc	384
	Gln Asp Gly Glu Phe Ile Tyr Lys Val Lys Leu Arg Gly Thr Asn Phe	
	115 120 125	
65	ccc tcc gac ggc ccc gta atg cag aag aag acc atg ggc tgg gag gcc	432
	Pro Ser Asp Gly Pro Val Met Gln Lys Lys Thr Met Gly Trp Glu Ala	
	130 135 140	

	tcc acc gag cgg atg tac ccc gag gac ggc gcc ctg aag ggc gag atc	480
	Ser Thr Glu Arg Met Tyr Pro Glu Asp Gly Ala Leu Lys Gly Glu Ile	
	145                      150                      155                      160	
5	aag atg agg ctg aag ctg aag gac	504
	Lys Met Arg Leu Lys Leu Lys Asp	
	165	
10	RFP F2E, Met added @ pos. 1 (RFP F2E corresponds to aa residues 170-225(end) of mRFP) SEQ ID NOS:1038 & 1039	
	atg ggc ggc cac tac gac gcc gag gtc aag acc acc tac atg gcc aag	48
15	Met Gly Gly His Tyr Asp Ala Glu Val Lys Thr Thr Tyr Met Ala Lys	
	1                      5                      10                      15	
	aag ccc gtg cag ctg ccc ggc gcc tac aag acc gac atc aag ctg gac	96
20	Lys Pro Val Gln Leu Pro Gly Ala Tyr Lys Thr Asp Ile Lys Leu Asp	
	20                      25                      30	
	atc acc tcc cac aac gag gac tac acc atc gtg gaa cag tac gag cgc	144
25	Ile Thr Ser His Asn Glu Asp Tyr Thr Ile Val Glu Gln Tyr Glu Arg	
	35                      40                      45	
	gcc gag ggc cgc cac tcc acc ggc gcc	171
	Ala Glu Gly Arg His Ser Thr Gly Ala	
	50                      55	
30	RFP F1F, pos. 1 Met removed (RFP F1F corresponds to aa residues 1-184 of mRFP) SEQ ID NOS:1040 & 1041	
	gcc tcc tcc gag gac gtc atc aag gag ttc atg cgc ttc aag gtg cgc	48
35	Ala Ser Ser Glu Asp Val Ile Lys Glu Phe Met Arg Phe Lys Val Arg	
	1                      5                      10                      15	
	atg gag ggc tcc gtg aac ggc cac gag ttc gag atc gag ggc gag ggc	96
40	Met Glu Gly Ser Val Asn Gly His Glu Phe Glu Ile Glu Gly Glu Gly	
	20                      25                      30	
	gag ggc cgc ccc tac gag ggc acc cag acc gcc aag ctg aag gtg acc	144
45	Glu Gly Arg Pro Tyr Glu Gly Thr Gln Thr Ala Lys Leu Lys Val Thr	
	35                      40                      45	
	aag ggc ggc ccc ctg ccc ttc gcc tgg gac atc ctg tcc cct cag ttc	192
	Lys Gly Gly Pro Leu Pro Phe Ala Trp Asp Ile Leu Ser Pro Gln Phe	
	50                      55                      60	
50	cag tac ggc tcc aag gcc tac gtg aag cac ccc gcc gac atc ccc gac	240
	Gln Tyr Gly Ser Lys Ala Tyr Val Lys His Pro Ala Asp Ile Pro Asp	
	65                      70                      75                      80	
55	tac ttg aag ctg tcc ttc ccc gag ggc ttc aag tgg gag cgc gtg atg	288
	Tyr Leu Lys Leu Ser Phe Pro Glu Gly Phe Lys Trp Glu Arg Val Met	
	85                      90                      95	

	aac ttc gag gac ggc ggc gtg gtg acc gtg acc cag gac tcc tcc ctg	336
	Asn Phe Glu Asp Gly Gly Val Val Thr Val Thr Gln Asp Ser Ser Leu	
	100 105 110	
5		
	cag gac ggc gag ttc atc tac aag gtg aag ctg cgc ggc acc aac ttc	384
	Gln Asp Gly Glu Phe Ile Tyr Lys Val Lys Leu Arg Gly Thr Asn Phe	
	115 120 125	
10		
	ccc tcc gac ggc ccc gta atg cag aag aag acc atg ggc tgg gag gcc	432
	Pro Ser Asp Gly Pro Val Met Gln Lys Lys Thr Met Gly Trp Glu Ala	
	130 135 140	
15		
	tcc acc gag cgg atg tac ccc gag gac ggc gcc ctg aag ggc gag atc	480
	Ser Thr Glu Arg Met Tyr Pro Glu Asp Gly Ala Leu Lys Gly Glu Ile	
	145 150 155 160	
20		
	aag atg agg ctg aag ctg aag gac ggc ggc cac tac gac gcc gag gtc	528
	Lys Met Arg Leu Lys Leu Lys Asp Gly Gly His Tyr Asp Ala Glu Val	
	165 170 175	
25		
	aag acc acc tac atg gcc aag	549
	Lys Thr Thr Tyr Met Ala Lys	
	180	
30		
	RFP F2F, Met added @ pos. 1	
	(RFP F2F corresponds to aa residues 185-225(end) of mRFP)	
	SEQ ID NOS:1042 & 1043	
	atg aag ccc gtg cag ctg ccc ggc gcc tac aag acc gac atc aag ctg	48
	Met Lys Pro Val Gln Leu Pro Gly Ala Tyr Lys Thr Asp Ile Lys Leu	
	1 5 10 15	
35		
	gac atc acc tcc cac aac gag gac tac acc atc gtg gaa cag tac gag	96
	Asp Ile Thr Ser His Asn Glu Asp Tyr Thr Ile Val Glu Gln Tyr Glu	
	20 25 30	
40		
	cgc gcc gag ggc cgc cac tcc acc ggc gcc	126
	Arg Ala Glu Gly Arg His Ser Thr Gly Ala	
	35 40	
45		
	KFP F1A, pos. 1 Met removed	
	(KFP F1A corresponds to aa residues 1-36 of KFP1)	
	SEQ ID NOS:1044 & 1045	
50		
	gcc tcc ctg ctg acc gag acc atg ccc ttc aag acc acc atc gag ggc	48
	Ala Ser Leu Leu Thr Glu Thr Met Pro Phe Lys Thr Thr Ile Glu Gly	
	1 5 10 15	
	acc gtg aac ggc cac tgc ttc aag tgc atc ggc aag ggc gag ggc aac	96
	Thr Val Asn Gly His Cys Phe Lys Cys Ile Gly Lys Gly Glu Gly Asn	
	20 25 30	
55		
	ccc ttc gag	105
	Pro Phe Glu	
	35	

KFP F2A, Met added @ pos. 1

(KFP F2A corresponds to aa residues 37-end of KFP1)

5 SEQ ID NOS:1046 & 1047

	atg ggc acc cag gag atg aag atc gag gtg atc gag ggc ggc ccc ctg	48
	Met Gly Thr Gln Glu Met Lys Ile Glu Val Ile Glu Gly Gly Pro Leu	
	1 5 10 15	
10	ccc ttc gcc ttc cac atc ctg tcc acc tcc tgc atg tac ggc tcc aag	96
	Pro Phe Ala Phe His Ile Leu Ser Thr Ser Cys Met Tyr Gly Ser Lys	
	20 25 30	
15	acc ttc atc aag tac gtg tcc ggc atc ccc gac tac ttc aag cag tcc	144
	Thr Phe Ile Lys Tyr Val Ser Gly Ile Pro Asp Tyr Phe Lys Gln Ser	
	35 40 45	
20	ttc ccc gag ggc ttc acc tgg gag cgc acc acc acc tac gag gac ggc	192
	Phe Pro Glu Gly Phe Thr Trp Glu Arg Thr Thr Thr Tyr Glu Asp Gly	
	50 55 60	
25	ggc ttc ctg acc gcc cac cag gac acc tcc ctg gac ggc gac tgc ctg	240
	Gly Phe Leu Thr Ala His Gln Asp Thr Ser Leu Asp Gly Asp Cys Leu	
	65 70 75 80	
30	gtg tac aag gtg aag atc ctg ggt aac aac ttc ccc gcc gac ggc ccc	288
	Val Tyr Lys Val Lys Ile Leu Gly Asn Asn Phe Pro Ala Asp Gly Pro	
	85 90 95	
35	gtg atg cag aac aag gtc ggc cgc tgg gag ccc gga acc gag atc gtg	336
	Val Met Gln Asn Lys Val Gly Arg Trp Glu Pro Gly Thr Glu Ile Val	
	100 105 110	
40	tac gag gtg gac ggc gtg ctg cgc ggc cag tcc ctg atg gcc ctg aag	384
	Tyr Glu Val Asp Gly Val Leu Arg Gly Gln Ser Leu Met Ala Leu Lys	
	115 120 125	
45	tgc ccc ggc ggc cgc cac ctg acc tgc cac ctg cac acc acc tac cgc	432
	Cys Pro Gly Gly Arg His Leu Thr Cys His Leu His Thr Thr Tyr Arg	
	130 135 140	
50	tcc aag aag ccc gcc tcc gcc ctg aag atg ccc ggc ttc cac ttc gag	480
	Ser Lys Lys Pro Ala Ser Ala Leu Lys Met Pro Gly Phe His Phe Glu	
	145 150 155 160	
55	gac cac cgc atc gag atc atg gag gag gtg gag aag ggc aag tgc tac	528
	Asp His Arg Ile Glu Ile Met Glu Glu Val Glu Lys Gly Lys Cys Tyr	
	165 170 175	
60	aag cag tac gag gcc gcc gtg ggc cgc tac tgc gac gcc gcc ccc tcc	576
	Lys Gln Tyr Glu Ala Ala Val Gly Arg Tyr Cys Asp Ala Ala Pro Ser	
	180 185 190	
65	aag ctg ggc cac aac	591
	Lys Leu Gly His Asn	
	195	

KFP F1B, pos. 1 Met removed

(KFP F1B corresponds to aa residues 1-98 of KFP1)

5 SEQ ID NOS:1048 & 1049

10	gcc tcc ctg ctg acc gag acc atg ccc ttc aag acc acc atc gag ggc Ala Ser Leu Leu Thr Glu Thr Met Pro Phe Lys Thr Thr Ile Glu Gly 1 5 10 15	48
15	acc gtg aac ggc cac tgc ttc aag tgc atc ggc aag ggc gag ggc aac Thr Val Asn Gly His Cys Phe Lys Cys Ile Gly Lys Gly Glu Gly Asn 20 25 30	96
20	ccc ttc gag ggc acc cag gag atg aag atc gag gtg atc gag ggc ggc Pro Phe Glu Gly Thr Gln Glu Met Lys Ile Glu Val Ile Glu Gly Gly 35 40 45	144
25	ccc ctg ccc ttc gcc ttc cac atc ctg tcc acc tcc tgc atg tac ggc Pro Leu Pro Phe Ala Phe His Ile Leu Ser Thr Ser Cys Met Tyr Gly 50 55 60	192
30	tcc aag acc ttc atc aag tac gtg tcc ggc atc ccc gac tac ttc aag Ser Lys Thr Phe Ile Lys Tyr Val Ser Gly Ile Pro Asp Tyr Phe Lys 65 70 75 80	240
35	cag tcc ttc ccc gag ggc ttc acc tgg gag cgc acc acc acc tac gag Gln Ser Phe Pro Glu Gly Phe Thr Trp Glu Arg Thr Thr Thr Tyr Glu 85 90 95	288
40	gac Asp	291

35 KFP F2B, Met added @ pos. 1

(KFP F2B corresponds to aa residues 99-end of KFP1)

SEQ ID NOS:1050 & 1051

40	atg ggc ggc ttc ctg acc gcc cac cag gac acc tcc ctg gac ggc gac Met Gly Gly Phe Leu Thr Ala His Gln Asp Thr Ser Leu Asp Gly Asp 1 5 10 15	48
45	tgc ctg gtg tac aag gtg aag atc ctg ggt aac aac ttc ccc gcc gac Cys Leu Val Tyr Lys Val Lys Ile Leu Gly Asn Asn Phe Pro Ala Asp 20 25 30	96
50	ggc ccc gtg atg cag aac aag gtc ggc cgc tgg gag ccc gga acc gag Gly Pro Val Met Gln Asn Lys Val Gly Arg Trp Glu Pro Gly Thr Glu 35 40 45	144
55	atc gtg tac gag gtg gac ggc gtg ctg cgc ggc cag tcc ctg atg gcc Ile Val Tyr Glu Val Asp Gly Val Leu Arg Gly Gln Ser Leu Met Ala 50 55 60	192
60	ctg aag tgc ccc ggc ggc cgg cac ctg acc tgc cac ctg cac acc acc Leu Lys Cys Pro Gly Gly Arg His Leu Thr Cys His Leu His Thr Thr 65 70 75 80	240

	tac cgc tcc aag aag ccc gcc tcc gcc ctg aag atg ccc ggc ttc cac	288
	Tyr Arg Ser Lys Lys Pro Ala Ser Ala Leu Lys Met Pro Gly Phe His	
	85 90 95	
5	ttc gag gac cac cgc atc gag atc atg gag gag gtg gag aag ggc aag	336
	Phe Glu Asp His Arg Ile Glu Ile Met Glu Glu Val Glu Lys Gly Lys	
	100 105 110	
10	tgc tac aag cag tac gag gcc gcc gtg ggc cgc tac tgc gac gcc gcc	384
	Cys Tyr Lys Gln Tyr Glu Ala Ala Val Gly Arg Tyr Cys Asp Ala Ala	
	115 120 125	
15	ccc tcc aag ctg ggc cac aac	405
	Pro Ser Lys Leu Gly His Asn	
	130 135	
20	KFP F1C, pos. 1 Met removed (KFP F1C corresponds to aa residues 1-153 of KFP1) SEQ ID NOS:1052 & 1053	
25	gcc tcc ctg ctg acc gag acc atg ccc ttc aag acc acc atc gag ggc	48
	Ala Ser Leu Leu Thr Glu Thr Met Pro Phe Lys Thr Thr Ile Glu Gly	
	1 5 10 15	
30	acc gtg aac ggc cac tgc ttc aag tgc atc ggc aag ggc gag ggc aac	96
	Thr Val Asn Gly His Cys Phe Lys Cys Ile Gly Lys Gly Glu Gly Asn	
	20 25 30	
35	ccc ttc gag ggc acc cag gag atg aag atc gag gtg atc gag ggc ggc	144
	Pro Phe Glu Gly Thr Gln Glu Met Lys Ile Glu Val Ile Glu Gly Gly	
	35 40 45	
40	ccc ctg ccc ttc gcc ttc cac atc ctg tcc acc tcc tgc atg tac ggc	192
	Pro Leu Pro Phe Ala Phe His Ile Leu Ser Thr Ser Cys Met Tyr Gly	
	50 55 60	
45	tcc aag acc ttc atc aag tac gtg tcc ggc atc ccc gac tac ttc aag	240
	Ser Lys Thr Phe Ile Lys Tyr Val Ser Gly Ile Pro Asp Tyr Phe Lys	
	65 70 75 80	
50	cag tcc ttc ccc gag ggc ttc acc tgg gag cgc acc acc acc tac gag	288
	Gln Ser Phe Pro Glu Gly Phe Thr Trp Glu Arg Thr Thr Thr Tyr Glu	
	85 90 95	
55	gac ggc ggc ttc ctg acc gcc cac cag gac acc tcc ctg gac ggc gac	336
	Asp Gly Gly Phe Leu Thr Ala His Gln Asp Thr Ser Leu Asp Gly Asp	
	100 105 110	
60	tgc ctg gtg tac aag gtg aag atc ctg ggt aac aac ttc ccc gcc gac	384
	Cys Leu Val Tyr Lys Val Lys Ile Leu Gly Asn Asn Phe Pro Ala Asp	
	115 120 125	
65	ggc ccc gtg atg cag aac aag gtc ggc cgc tgg gag ccc gga acc gag	432
	Gly Pro Val Met Gln Asn Lys Val Gly Arg Trp Glu Pro Gly Thr Glu	
	130 135 140	



atc gtg tac gag gtg gac ggc gtg 456  
 Ile Val Tyr Glu Val Asp Gly Val  
 145 150  
 5  
 KFP F2C, Met added @ pos. 1  
 (KFP F2C corresponds to aa residues 154-end of KFP1)  
 SEQ ID NOS:1054 & 1055  
 10  
 atg ctg cgc ggc cag tcc ctg atg gcc ctg aag tgc ccc ggc ggc cgg 48  
 Met Leu Arg Gly Gln Ser Leu Met Ala Leu Lys Cys Pro Gly Gly Arg  
 1 5 10 15  
 15  
 cac ctg acc tgc cac ctg cac acc acc tac cgc tcc aag aag ccc gcc 96  
 His Leu Thr Cys His Leu His Thr Thr Tyr Arg Ser Lys Lys Pro Ala  
 20 25 30  
 20  
 tcc gcc ctg aag atg ccc ggc ttc cac ttc gag gac cac cgc atc gag 144  
 Ser Ala Leu Lys Met Pro Gly Phe His Phe Glu Asp His Arg Ile Glu  
 35 40 45  
 25  
 atc atg gag gag gtg gag aag ggc aag tgc tac aag cag tac gag gcc 192  
 Ile Met Glu Glu Val Glu Lys Gly Lys Cys Tyr Lys Gln Tyr Glu Ala  
 50 55 60  
 30  
 gcc gtg ggc cgc tac tgc gac gcc gcc ccc tcc aag ctg ggc cac aac 240  
 Ala Val Gly Arg Tyr Cys Asp Ala Ala Pro Ser Lys Leu Gly His Asn  
 65 70 75 80  
 KFP F1D, pos. 1 Met removed  
 (KFP F1D corresponds to aa residues 1-112 of KFP1)  
 SEQ ID NOS:1056 & 1057  
 35  
 gcc tcc ctg ctg acc gag acc atg ccc ttc aag acc acc atc gag ggc 48  
 Ala Ser Leu Leu Thr Glu Thr Met Pro Phe Lys Thr Thr Ile Glu Gly  
 1 5 10 15  
 40  
 acc gtg aac ggc cac tgc ttc aag tgc atc ggc aag ggc gag ggc aac 96  
 Thr Val Asn Gly His Cys Phe Lys Cys Ile Gly Lys Gly Glu Gly Asn  
 20 25 30  
 45  
 ccc ttc gag ggc acc cag gag atg aag atc gag gtg atc gag ggc ggc 144  
 Pro Phe Glu Gly Thr Gln Glu Met Lys Ile Glu Val Ile Glu Gly Gly  
 35 40 45  
 50  
 ccc ctg ccc ttc gcc ttc cac atc ctg tcc acc tcc tgc atg tac ggc 192  
 Pro Leu Pro Phe Ala Phe His Ile Leu Ser Thr Ser Cys Met Tyr Gly  
 50 55 60  
 55  
 tcc aag acc ttc atc aag tac gtg tcc ggc atc ccc gac tac ttc aag 240  
 Ser Lys Thr Phe Ile Lys Tyr Val Ser Gly Ile Pro Asp Tyr Phe Lys  
 65 70 75 80  
 55  
 cag tcc ttc ccc gag ggc ttc acc tgg gag cgc acc acc acc tac gag 288  
 Gln Ser Phe Pro Glu Gly Phe Thr Trp Glu Arg Thr Thr Thr Tyr Glu  
 85 90 95

	gac ggc ggc ttc ctg acc gcc cac cag gac acc tcc ctg gac ggc	333
	Asp Gly Gly Phe Leu Thr Ala His Gln Asp Thr Ser Leu Asp Gly	
	100 105 110	
5	KFP F2D, Met added @ pos. 1 (KFP F2D corresponds to aa residues 113-end of KFP1) SEQ ID NOS:1058 & 1059	
10	atg gac tgc ctg gtg tac aag gtg aag atc ctg ggt aac aac ttc ccc	48
	Met Asp Cys Leu Val Tyr Lys Val Lys Ile Leu Gly Asn Asn Phe Pro	
	1 5 10 15	
15	gcc gac ggc ccc gtg atg cag aac aag gtc ggc cgc tgg gag ccc gga	96
	Ala Asp Gly Pro Val Met Gln Asn Lys Val Gly Arg Trp Glu Pro Gly	
	20 25 30	
20	acc gag atc gtg tac gag gtg gac ggc gtg ctg cgc ggc cag tcc ctg	144
	Thr Glu Ile Val Tyr Glu Val Asp Gly Val Leu Arg Gly Gln Ser Leu	
	35 40 45	
25	atg gcc ctg aag tgc ccc ggc ggc cgg cac ctg acc tgc cac ctg cac	192
	Met Ala Leu Lys Cys Pro Gly Gly Arg His Leu Thr Cys His Leu His	
	50 55 60	
30	acc acc tac cgc tcc aag aag ccc gcc tcc gcc ctg aag atg ccc ggc	240
	Thr Thr Tyr Arg Ser Lys Lys Pro Ala Ser Ala Leu Lys Met Pro Gly	
	65 70 75 80	
35	ttc cac ttc gag gac cac cgc atc gag atc atg gag gag gtg gag aag	288
	Phe His Phe Glu Asp His Arg Ile Glu Ile Met Glu Glu Val Glu Lys	
	85 90 95	
40	ggc aag tgc tac aag cag tac gag gcc gcc gtg ggc cgc tac tgc gac	336
	Gly Lys Cys Tyr Lys Gln Tyr Glu Ala Ala Val Gly Arg Tyr Cys Asp	
	100 105 110	
45	gcc gcc ccc tcc aag ctg ggc cac aac	363
	Ala Ala Pro Ser Lys Leu Gly His Asn	
	115 120	
	KFP F1E, pos. 1 Met removed (KFP F1E corresponds to aa residues 1-169 of KFP1) SEQ ID NOS:1060 & 1061	
50	gcc tcc ctg ctg acc gag acc atg ccc ttc aag acc acc atc gag ggc	48
	Ala Ser Leu Leu Thr Glu Thr Met Pro Phe Lys Thr Thr Ile Glu Gly	
	1 5 10 15	
55	acc gtg aac ggc cac tgc ttc aag tgc atc ggc aag ggc gag ggc aac	96
	Thr Val Asn Gly His Cys Phe Lys Cys Ile Gly Lys Gly Glu Gly Asn	
	20 25 30	
60	ccc ttc gag ggc acc cag gag atg aag atc gag gtg atc gag ggc ggc	144
	Pro Phe Glu Gly Thr Gln Glu Met Lys Ile Glu Val Ile Glu Gly Gly	
	35 40 45	

	ccc ctg ccc ttc gcc ttc cac atc ctg tcc acc tcc tgc atg tac ggc	192
	Pro Leu Pro Phe Ala Phe His Ile Leu Ser Thr Ser Cys Met Tyr Gly	
	50 55 60	
5	tcc aag acc ttc atc aag tac gtg tcc ggc atc ccc gac tac ttc aag	240
	Ser Lys Thr Phe Ile Lys Tyr Val Ser Gly Ile Pro Asp Tyr Phe Lys	
	65 70 75 80	
10	cag tcc ttc ccc gag ggc ttc acc tgg gag cgc acc acc acc tac gag	288
	Gln Ser Phe Pro Glu Gly Phe Thr Trp Glu Arg Thr Thr Thr Tyr Glu	
	85 90 95	
15	gac ggc ggc ttc ctg acc gcc cac cag gac acc tcc ctg gac ggc gac	336
	Asp Gly Gly Phe Leu Thr Ala His Gln Asp Thr Ser Leu Asp Gly Asp	
	100 105 110	
20	tgc ctg gtg tac aag gtg aag atc ctg ggt aac aac ttc ccc gcc gac	384
	Cys Leu Val Tyr Lys Val Lys Ile Leu Gly Asn Asn Phe Pro Ala Asp	
	115 120 125	
25	ggc ccc gtg atg cag aac aag gtc ggc cgc tgg gag ccc gga acc gag	432
	Gly Pro Val Met Gln Asn Lys Val Gly Arg Trp Glu Pro Gly Thr Glu	
	130 135 140	
30	atc gtg tac gag gtg gac ggc gtg ctg cgc ggc cag tcc ctg atg gcc	480
	Ile Val Tyr Glu Val Asp Gly Val Leu Arg Gly Gln Ser Leu Met Ala	
	145 150 155 160	
35	ctg aag tgc ccc ggc ggc cgg cac	504
	Leu Lys Cys Pro Gly Arg His	
	165	
40	atg ctg acc tgc cac ctg cac acc acc tac cgc tcc aag aag ccc gcc	48
	Met Leu Thr Cys His Leu His Thr Thr Tyr Arg Ser Lys Lys Pro Ala	
	1 5 10 15	
45	tcc gcc ctg aag atg ccc ggc ttc cac ttc gag gac cac cgc atc gag	96
	Ser Ala Leu Lys Met Pro Gly Phe His Phe Glu Asp His Arg Ile Glu	
	20 25 30	
50	atc atg gag gag gtg gag aag ggc aag tgc tac aag cag tac gag gcc	144
	Ile Met Glu Glu Val Glu Lys Gly Lys Cys Tyr Lys Gln Tyr Glu Ala	
	35 40 45	
55	gcc gtg ggc cgc tac tgc gac gcc gcc ccc tcc aag ctg ggc cac aac	192
	Ala Val Gly Arg Tyr Cys Asp Ala Ala Pro Ser Lys Leu Gly His Asn	
	50 55 60	

KFP F2E, Met added @ pos. 1  
(KFP F2E corresponds to aa residues 170-end of KFP1)  
SEQ ID NOS:1062 & 1063

KFP F1F, pos. 1 Met removed  
(KFP F1F corresponds to aa residues 1-186 of KFP1)  
SEQ ID NOS:1064 & 1065

5	gcc tcc ctg ctg acc gag acc atg ccc ttc aag acc acc atc gag ggc Ala Ser Leu Leu Thr Glu Thr Met Pro Phe Lys Thr Thr Ile Glu Gly 1 5 10 15	48
10	acc gtg aac ggc cac tgc ttc aag tgc atc ggc aag ggc gag ggc aac Thr Val Asn Gly His Cys Phe Lys Cys Ile Gly Lys Gly Glu Gly Asn 20 25 30	96
15	ccc ttc gag ggc acc cag gag atg aag atc gag gtg atc gag ggc ggc Pro Phe Glu Gly Thr Gln Glu Met Lys Ile Glu Val Ile Glu Gly Gly 35 40 45	144
20	ccc ctg ccc ttc gcc ttc cac atc ctg tcc acc tcc tgc atg tac ggc Pro Leu Pro Phe Ala Phe His Ile Leu Ser Thr Ser Cys Met Tyr Gly 50 55 60	192
25	tcc aag acc ttc atc aag tac gtg tcc ggc atc ccc gac tac ttc aag Ser Lys Thr Phe Ile Lys Tyr Val Ser Gly Ile Pro Asp Tyr Phe Lys 65 70 75 80	240
30	cag tcc ttc ccc gag ggc ttc acc tgg gag cgc acc acc acc tac gag Gln Ser Phe Pro Glu Gly Phe Thr Trp Glu Arg Thr Thr Thr Tyr Glu 85 90 95	288
35	gac ggc ggc ttc ctg acc gcc cac cag gac acc tcc ctg gac ggc gac Asp Gly Gly Phe Leu Thr Ala His Gln Asp Thr Ser Leu Asp Gly Asp 100 105 110	336
40	tgc ctg gtg tac aag gtg aag atc ctg ggt aac aac ttc ccc gcc gac Cys Leu Val Tyr Lys Val Lys Ile Leu Gly Asn Asn Phe Pro Ala Asp 115 120 125	384
45	ggc ccc gtg atg cag aac aag gtc ggc cgc tgg gag ccc gga acc gag Gly Pro Val Met Gln Asn Lys Val Gly Arg Trp Glu Pro Gly Thr Glu 130 135 140	432
50	atc gtg tac gag gtg gac ggc gtg ctg cgc ggc cag tcc ctg atg gcc Ile Val Tyr Glu Val Asp Gly Val Leu Arg Gly Gln Ser Leu Met Ala 145 150 155 160	480
55	ctg aag tgc ccc ggc ggc cgg cac ctg acc tgc cac ctg cac acc acc Leu Lys Cys Pro Gly Gly Arg His Leu Thr Cys His Leu His Thr Thr 165 170 175	528
60	tac cgc tcc aag aag ccc gcc tcc gcc Tyr Arg Ser Lys Lys Pro Ala Ser Ala 180 185	555

KFP F2F, Met added @ pos. 1

KFP F2F corresponds to aa residues 187-end of KFP1)

SEQ ID NOS:1066 & 1067

```
5  atg ctg aag atg ccc ggc ttc cac ttc gag gac cac cgc atc gag atc      48
   Met Leu Lys Met Pro Gly Phe His Phe Glu Asp His Arg Ile Glu Ile
   1             5             10             15

10 atg gag gag gtg gag aag ggc aag tgc tac aag cag tac gag gcc gcc      96
   Met Glu Glu Val Glu Lys Gly Lys Cys Tyr Lys Gln Tyr Glu Ala Ala
       20             25             30

   gtg ggc cgc tac tgc gac gcc gcc ccc tcc aag ctg ggc cac aac      141
   Val Gly Arg Tyr Cys Asp Ala Ala Pro Ser Lys Leu Gly His Asn
   15       35             40             45
```

Unmutated fragments that form a part of the invention:

20 ["aa" = amino acid]

GFP F1: aa residues 1-39 of wt GFP (SEQ ID NO:2);

GFP F2: aa residues 40-238 of wt GFP(SEQ ID NO:2);

```
25 YFP F1A: aa residues 1-40 of EYFP(SEQ ID NO:4);
   YFP F2A: aa residues 41-239 of EYFP(SEQ ID NO:4);
   YFP F1B: aa residues 1-103 of EYFP(SEQ ID NO:4);
   YFP F2B: aa residues 104-239 of EYFP(SEQ ID NO:4);
   YFP F1C: aa residues 1-117 of EYFP(SEQ ID NO:4);
30 YFP F2C: aa residues 118-239 of EYFP(SEQ ID NO:4);
   YFP F1DX: aa residues 1-158 of EYFP(SEQ ID NO:4);
   YFP F2DX: aa residues 159-239 of EYFP(SEQ ID NO:4);
   YFP F1D: aa residues 1-159 of EYFP(SEQ ID NO:4);
   YFP F2D: aa residues 160-239 of EYFP(SEQ ID NO:4);
35 YFP F1E: aa residues 1-174 of EYFP(SEQ ID NO:4);
   YFP F2E: aa residues 175-239 of EYFP(SEQ ID NO:4);
   YFP F1F: aa residues 1-191 of EYFP(SEQ ID NO:4);
   YFP F2F: aa residues 192-239 of EYFP(SEQ ID NO:4);
```

40 EGFPF2A: aa residues 41-239 of EGFP (SEQ ID NO:3);

RFP F1A: aa residues 1-39 of mRFP(SEQ ID NOS:15 & 16);

RFP F2A: aa residues 40-225 of mRFP(SEQ ID NOS:15 & 16);

RFP F1B: aa residues 1-101 of mRFP(SEQ ID NOS:15 & 16);

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45 RFP F2B: aa residues 102-225 of mRFP(SEQ ID NOS:15 & 16);
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RFP F1C: aa residues 1-115 of mRFP(SEQ ID NOS:15 & 16);

RFP F2C: aa residues 116-225 of mRFP(SEQ ID NOS:15 & 16);

RFP F1D: aa residues 1-153 of mRFP(SEQ ID NOS:15 & 16);

RFP F2D: aa residues 154-225 of mRFP(SEQ ID NOS:15 & 16);

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50 RFP F1E: aa residues 1-169 of mRFP(SEQ ID NOS:15 & 16);
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RFP F2E: aa residues 170-225 of mRFP(SEQ ID NOS:15 & 16);

RFP F1F: aa residues 1-184 of mRFP(SEQ ID NOS:15 & 16);

RFP F2F: aa residues 185-225 of mRFP(SEQ ID NOS:15 & 16);

55 KFP F1A: aa residues 1-36 of KFP1(SEQ ID NOS:17 & 18);

KFP F2A: aa residues 37-232 of KFP1(SEQ ID NOS:17 & 18);

KFP F1B: aa residues 1-98 of KFP1(SEQ ID NOS:17 & 18);

KFP F2B: aa residues 99-232 of KFP1(SEQ ID NOS:17 & 18);  
KFP F1C: aa residues 1-153 of KFP1(SEQ ID NOS:17 & 18);  
KFP F2C: aa residues 154-232 of KFP1(SEQ ID NOS:17 & 18);  
5 KFP F1D: aa residues 1-112 of KFP1(SEQ ID NOS:17 & 18);  
KFP F2D: aa residues 113-232 of KFP1(SEQ ID NOS:17 & 18);  
KFP F1E: aa residues 1-169 of KFP1(SEQ ID NOS:17 & 18);  
KFP F2E: aa residues 170-232 of KFP1(SEQ ID NOS:17 & 18);  
KFP F1F: aa residues 1-186 of KFP1(SEQ ID NOS:17 & 18);  
10 KFP F2F: aa residues 187-232 of KFP1(SEQ ID NOS:17 & 18).

15

20

While the many forms of the invention herein disclosed constitute presently preferred embodiments, many others are possible and further details of the preferred embodiments and other possible embodiments are not to be construed as limitations. It is understood that the terms  
5 used herein are merely descriptive rather than limiting and that various changes many equivalents may be made without departing from the spirit or scope of the claimed invention.